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/label- Pro_peptide
/note- "Pro sequence of RP-II protease"
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/label= Signal_peptide
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                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435...
420.5
419.5
417
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                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sednence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                                        on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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9
                                                                                                                                                                                                                                     Run
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protease"

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/note= "Bacillus pumilus BO32 mature RP-II
                                                                                                                                                                                                                   N-PSDB; AAD03002
                                                                                                                                                                               Flensted Lassen
                         WO200116285-A2
                                                                         31-AUG-2000;
                                                                                                             20-OCT-1999;
                                                                                                   31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||
302-ag 303
                                               08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE00196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residual protease II; RP-II; additive; cleaning composition; detergent
                                                                                                                                                                           combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                      The present sequence is Bacillus pumilus JA96 RP-II (Residual protease II). RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 redtnlayytldtfsgnsgsamldqnqqivgvhnagysngtinggpkataafvefinyak 300
                                                                                                                                                                                                                                                                                                                                                                                                               GTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGYINTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFINYAK 300
                                                                                                                                                                                                                                                                                                                                                                                                 DKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCT 120
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                           ţ,
                                                                                                                                                                                                                                                                                                                                                 1 MKKVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSF 60
                                                                                                                                                                                                                                                                                                                                                               constituents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQYDFAVIKTDTNIGNTVGYRSIRQYTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVT
 Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                             Length 302;
                                                                          Novel RP-II type protease and its variants useful as constiguentergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27..88
/label- Pro_peptide
/note- "Pro sequence of RP-II protease"
89..303
                                                                                                                                                                                                                                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                         .;
0
                                                                                                                                                                                                                                                                                              Score 1559; DB 22;
Pred. No. 1.5e-116;
Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...26
'label= Signal_peptide
                                                                                                                 Claim 1; Page 119-120; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus pumilus BO32 RP-II protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE00014 standard; Protein; 303 AA
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                              100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                       Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B032
Norregaard-madsen M,
Flensted Lassen S;
                                      2001-226680/23
                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                         302 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pumilus
                                                  N-PSDB; AAD03004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aq 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus
                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                  The present sequence is Bacillus pumilus B032 RP-II (Residual protease II). RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, ceilulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 REDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHAAGYSNGTINGGPKATAAFVEFINYAK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTLIAPHKILTRAHCVYNTAFRSYSAKGSVYPGANISTAVNÓSANATERTVPSGTINTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 redtnlayymidtfsgnsgsamldqnqqivqvhnagysngtinggpkataafvefinyak 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel RP-II type protease and its variants useful as constituents in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKKVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 mkkvkmllpsllvfgalsvpsfahaasdsvltsdydmvtsdgkvisssdfhndtkspssf 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQYDFAVIKTDTNIGNTVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVT
                                                                                                                                            Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 303;
                                                                                                                                                                                                                                                                                         detergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1506; DB 22;
Pred. No. 2.6e-112;
; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4188
                                                                                                                                            Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 112-113; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 05X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein; 215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                      99DK-0001212.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.6%;
95.7%;
2000WO-DK00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                          Norregaard-madsen M,
                                                                                                   (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                         WPI; 2001-226680/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE00196 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 AA;
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31-AUG-1999;
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                                                                                                                                                                                  31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2001
                                                                                                                                               AAE00197;
                                                                                                              AAE00197
                                                                                                                                                                                                                                                  Residual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                  AAE00197
                                                                               RESULT
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                               Residual protease II; RP-II; additive; cleaning composition; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificaties, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GSVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 VVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ
                                                                                                                                                                                                                                                                                                                                                                                   Rahbek Ostergaard P, Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present_sequence is Bacillus pumilus (JA96) RP-II protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 215;
                                                                                                                                                               /note= "Wild type Glu substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1118; DB 22;
Pred. No. 1.5e-81;
Bacillus pumilus RP-II protease variant (E155A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                         ^{n \sim I} Location/Qualifiers Misc-difference 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                99DK-0001212 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.78;
99.58;
                                                                                                                                                                                                                                                               31-AUG-2000; 2000WO-DK00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                  mutant; mutein; variant.
                                                                               Sacillus pumilus JA96
                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                   Norregaard-madsen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-226680/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 AA;
                                                                                                                                                                                               WO200116285-A2
                                                                                                                                                                                                                                                                                                31-AUG-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peroxidase.
                                                                                                                                                                                                                                  DB-MAR-2001
                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         802
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Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein [SEO ID NO: 2] shown in page 101-102 of the specification (AABDOIL). The specification also refers to following variants: (a) VIF, (b) D7G+T1255*E152G+N1821, (c) S119A+S144T+Q157R+S1751, (d) H141A, (e) E152A+Q122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), His residue in (d), Gin residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protease II; RP-II; additive; cleaning composition; detergent; nutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constituents in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel RP-II type protease and its variants useful as constit detergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Glu substituted with Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.6%; Score 1117; DB 22;
99.5%; Pred. No. 1.8e-81;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus pumilus RP-II protease variant (E155G)
Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                            standard; Protein; 215 AA.
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Matches 214; Conservative
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutant; mutein;
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20-OCT-1999;
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Matches 214;
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                                                                                                                                                                                                                                                                                                                                                                                     Residual protease II; RP-II; additive; cleaning composition; detergent; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein (SEQ ID NO: 2) shown in page 101-102 of the specification (AAE00011). The specification also
                                                                 207
                                                                                           120
                                                                                                                       267
                                                                                                                                   Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions \, -
            VVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAK
                           GSVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT
                                                                                 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is Bacillus pumilus (JA96) RP-II protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- "Wild type Asp substituted with Gly"
                                                                                                                                                                                                                                                                                                                                                              Bacillus pumilus RP-II protease variant (D156G)
                                                                                                                                                                                           QIVGVHNAGYSNGTINGGPKATAAFVEFINYAKAQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rahbek Ostergaard P,
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156
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus pumilus JA96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-2000;
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20-OCT-1999;
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              88
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refers to following variants: (a) V1F, (b) D7G+T125S+E152G+N182I, (c) S119A+S144T+Q157R+S175I, (d) H141A. (e) E152A+Q122R, (f) N18ZT+C185A, (g) E15ZA+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), H1s residue in (d), Gln residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                se II; RP-II; additive; cleaning composition; detergent; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                              88 VVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAK 147
                                                                                                                                                                                                                                                                                                                                                                                                                   GSVYPCMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ 267
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                                                                                                                                                                                                                              Length 215;
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                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIVGVHNAGYSNGTINGGPKATAAFVEFINYAKAQ 302
                                                                                                                                                                                                                              Score 1117; DE
Pred. No. 1.8e-
0; Mismatches
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99.5%;
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                          Similarity
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                                                                                                                          Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein [SEO ID NO: 2] shown in page 101-102 of the specification (AAEOOIL). The specification also refers to following variants: (a) VIF, (b) D767F1255*E1526*N1821, (c) S119A+S1447+Q157R+S1751, (d) H141A, (e) E152A+Q122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), His residue in (d) and (f) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protease II; RP-II; additive; cleaning composition; detergent;
          The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions dother cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as such astalytic rate, stability, especially towards
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                                                                                                                                                                                                                                                                                                                                                                  the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                Length 215;
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                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus pumilus RP-II professe variant (E155A+D156A)
                                                                                                                                                                                                                                                                                                 Score 1116; DB 22;
Pred. No. 2.2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QIVGVHNAGYSNGTINGGPKATAAFVEFINYAKAQ 302
                                                                                                                                                                                                                                                                                                                           0; Mismatches
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99.5%;
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Best Local Similarity
                                                                                                                                                                                                                                                             215 AA;
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                                                                                                                 peroxidase.
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Synthetic.
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Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein (SEQ ID NO: 2) shown in page 101-102 of the specification (AAEOOIL). The specification also refers to following variants: (a) VIF, (b) D764712554E152G+N1821, (c) S119A+S1447+O157R+S1751, (d) H141A, (e) E152A+O122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), His residue in (d), Gln residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 GSVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constituents in
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is Bacillus pumilus (JA96) RP-II protease variant (E155A+D156A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 215;
                                                                                                                                                                                                                                                                               Novel RP-II type protease and its variants useful as constited detergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1110; DB 22;
Pred. No. 6.7e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus licheniformis CDJ31 RP-II protease.
                                                                                                                           Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE00015 standard; Protein; 318
99DK-0001500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.28;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus licheniformis CDJ31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 213; Conservative
                                                             (NOVO ) NOVOZYMES AS
                                                                                                                           Norregaard-madsen M,
                                                                                                                                                                                                                     WPI; 2001-226680/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                           Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00015;
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is Bacillus licheniformis CDJ31 RP-II (Residual protease II). RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-----PSSFDKVDDLSSTI-GEKVKPL--TTYLKDFQTKVVIGDDGRTKVTNTRVAPY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANM 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VKKLIPSLLVFGALSVPSF-----AHAASDSVLTSDYDMVTSDG--KVISSADFHNDMK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel RP-II type protease and its variants useful as constituents detergent compositions, additives and cleaning compositions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-NLTGTTIKISGYPGDKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STGKVSQWEMSGPVTREDTNLAYYT1DTFSGNSGSAMLDQNQQ-----1VGVHNAG-
                                                                                              RP-II
                                                                                                                                                                                                                                                                                              Rahbek Ostergaard P, Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.9%; Score 435.5; DB 22; Length 318; Best Local Similarity 35.5%; Pred. No. 7.9e-27; Matches 111; Conservative 49; Mismatches 116; Indels 37;
                                                                    /note= "Pro sequence of RP-II protease" 97.318
/note= "Bacillus licheniformis CDJ31 mature protease"
                                    29..96
/label= Pro_peptide
/note= "Pro sequence of RP-II protease"
                           /label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 115-117; 132pp; English.
Location/Qualifiers
                                                                                                                                                                                                                        99DK-0001212 6
99DK-0001500.
                                                                                                                                                                                              2000WO-DK00476
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yggssynrgtr1t 303
                                                                                                                                                                                                                                                                                            Norregaard-madsen M,
Flensted Lassen S;
                                                                                                                                                                                                                                                                  (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-226680/23.
N-PSDB; AAD03003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AA;
                                                                                                                                    WO200116285-A2
                                                                                                                                                                                            31-AUG-2000;
                                                                                                                                                                                                                        31-AUG-1999;
20-OCT-1999;
                                                                                                                                                                  08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
 Key
Peptide
                                          Peptide
                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526
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                                                                                                                                                                                                                                                                                                                           g
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licheniformis designated Blase. Blase specifically cleaves the peptide hand at the carboxyl terminal of giutamic acid residues in amino acid sequence of polypeptides. The professe has an optimal join approx 8.0 with a stable ph range of 6.5-8.5. Blase is useful cleaving proteins to enable protein structural analysis or for separating componence of fusion proteins linked by a glutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g.
                                                                                                                                                                           pH range; protein structural analysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence give is a novel protease derived from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tamaki M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protease derived from Bacillus licheniformis - useful for sepg. fusion protein components by cleaving glutamic acid residues
Not Novortand Hove Nordish
                                                                                                                                                                                                                                                                                                       /label- OTHER
/note= "OTHER= formyl methionine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiwara T, Matsumoto K, Nakamura E,
Teraoka H, Tsuzuki H, Yoshida N;
                                                                                                                                                                                                                                                        /label= signal_peptide
95.316
/label= BLase_protein
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 19; 32pp; English.
                                                                                 AAR23730 standard; Protein; 316 AA
                                                                                                                                                                                                                                                                                                                                                                                      91EP-0309737.
                                                                                                                                                                                                                                                                                                                                                                                                             90JP-0288110.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (SHIO ) SHIONOGI & CO LTD. (SHIO ) SHIONOGI SEIYAKU KK.
                                                                                                                                 (first entry)
                                                                                                                                                                            BLase; glutamic acid;
fusion proteins; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-142934/18.
N-PSDB; AAQ24382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 AA;
                                                                                                                                                      Protease Blase
                                                                                                                                                                                                                                                                                             modified base
                                                                                                                              30-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                29-APR-1992
                                                                                                                                                                                                                                                                                                                                         EP482879-A
                                                                                                                                                                                                              Synthetic
                                                                                                        AAR23730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                       Key
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10;

Gaps 26 61

29;

DB 13; Length 316;

27.0%; Score 420.5; DB 13; Length 3 53.0%; Pred. No. 1.2e-25; ative 55; Mismatches 121; Indels

Query Match
Best Local Similarity 33.08
Matches 101; Conservative

57 ---PSSFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYIT 113

4 kksvkrglitgligisiyslgmhpa--qaapsphtpvssdpsykaetsvtydpn1ksdgy 5 KKLIPSLLVFGALSVPSFA---HAASDSVLTSDYDMVTSDG--KVISSADFHNDMKT---

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114 FGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPS 173

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Best Local Similarity
Matches 106; Conserv
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20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE00013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                  47
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                                                                                                                                                                                                                                                                                                                                                                226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residual protease II; RP-II; additive; cleaning composition; detergent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease II). RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.94
/label- Pro_peptide
/note- "Pro sequence of RP-II protease"
/note- "Bacillus licheniformis mature RP-II protease"
121 ssigsctgwmigpktvataghciydtssgsfagtatvspgrngtsypygsvkstryfips 180
                                                                                                              233 WEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQ-----IVGVHNAG-YSNGTIN 283
                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is Bacillus licheniformis (BLC) RP-II (Residual
                                     GYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-NLTGTTIKISGYPGDKMRSTGKVSQ
                                                         Novel RP-II type protease and its variants useful as constituents detergent compositions, additives and cleaning compositions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahbek Ostergaard P, Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus licheniformis (BLC) RP-II protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label- Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 101-102; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        AAE00011 standard; Protein; 316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99DK-0001212.V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-2000; 2000WO-DK00476.V
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norregaard-madsen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-226680/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD02999
                                                                                                                                                                                       284 GGPKAT 289
                                                                                                                                                                                                                 | : |
rgtrit 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #0200116285-A2
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20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                              AAE00011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                     174
                                                                                                                                                                                                                             296
                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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protease II; RP-II; additive; cleaning composition; detergent.
                                                                                                                                                     STGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQ-----IVGVHNAG- 276
                                                                                                                                                                                                                                                     NSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANM 166
                                                                                      SADFHNDMKTPSSFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPY 106
              Gaps
                                      -- YD-MVTSDGKVIS 46
                                                    Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions -
                                                                                                   | | : :| | | : :| | | | skaftgtgkvnetkek-----aekkspaka---pysiksvigsddrtrvtnttaypy
                                                                                                                                                                                        TEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-NLTGTTIKISGYPGDKMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Pro Sequence of RP-II protease"
93..314
/note= "Bacillus licheniformis AC116 mature RP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Voge Christensen CB;
              41;
             Indels
 Pred. No. 1.5e-25;
; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus licheniformis AC116 RP-II protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahbek Ostergaard P,
                                      2 KKVKK-LIPSLLVFGALSV---PSFAHAASDSVLTSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..29
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 109-110; 132pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30..92
/label-_Pro_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                 AAE00013 standard; Protein; 314
             46;
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33.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000; 2000WO-DK00476
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protease"
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus licheniformis.
                                                                                                                                                                                                                                                                                          277 YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                                                                 289 yggssynrgtrit 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norregaard-madsen M,
Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-226680/23.
N-PSDB; AAD03001.
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Norregaard-madsen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00036;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE00036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residual protease II; RP-II; additive; cleaning composition; detergent;
                    protease II). RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipses, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved
                                                                                                                                                                                                                                                                                                                             TGASQYDFAVIKTDTNIGNTVGYRSIR-QVTNLTGTTIKISGYPGDKMRSTGKVSQWEMS 236
                                                                                                                                                                                                                                                                                                                                        :| | ||:| |: |||||||| sgnsnydyaaielsqpigntvgyfgysytasslagagvtlsgypgdk--ttg--tqwqms 237
                                                                                                                                                                                                                                                           63 kafegtgtpggsvqakpkkespagppyspksvigsdertrvtdttafpyraivhisssig 122
                                                                                                                                                                                                                                                                                             GPVTREDINLAYYIIDIFSGNSGSAMLDQNQQ-----IVGVHNAG-YSNGTINGGPK 287
                                                                                                                                                                                                                                       59 -SFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGS 117
                                                                                                                                                                                                                                                                                  SCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGYIN 177
                                                                                                                                                                                                                                                                                                                                                                                             gtlavsetyklgyaidtygggsgspvyeksssrtncsgpcslavhtngvyggssynrgtr 297
                                                                                                                                                                                         5 KKLIPSLLVFGALSVPSFAHAA-SDSVLTSDYDMVTSDGKVISSADFHNDMKTPS----- 58
                                                                                                                                                                                                              3 kngvsrvfiagligisifssgiysaqaassphtpvssdpsykpgstydpnikidnngays 62
            sequence is Bacillus licheniformis AC116 RP-II (Residual
                                                                                                                                                                      22;
                                                                                                                                              Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild type Gly substituted with Arg'
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis RP-II protease variant (G55R)
                                                                                                                                                Score 417; DB 22;
Pred. No. 2.3e-25;
                                                                                                                                                                      54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE00075 standard; Protein; 222 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DK-0001212 5
                                                                                          resistance towards peroxidase
                                                                                                                                                26.7%;
33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-AUG-2000; 2000WO-DK00476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                      Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus licheniformis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVOZYMES AS.
                                                                                                                                                            Similarity
                                                                                                                 314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200116285-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2001
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20-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     288 AT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                          299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE00075;
                                                                                                                Sequence
                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         298 it
                                                                                                                                                              Best Local
                                                                                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                         123
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                                                                                                                                                                                                                                                                                                                                                     182
                                                                                                                                                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE00075
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Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein (SEQ ID NO: 2) shown in page 101-102 of the specification (AAEOOIL). The specification also refers to following variants: (a) VIF, (b) D76T1255-E1526-N1821, (c) S119A+S144T+Q157R+S1751, (d) H141A, (e) E152A+Q122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), His residue in (d), din residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residual protease II; RP-II; additive; cleaning composition; detergent;
                                                                                                                                                                                                                                                                                                                               corresponding nucleic acid sequences and variants. RP-11 protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-11 have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| || | :: || | ::|||| :||||| | 62 tvspgrngtsypygsvkstryfipsgw~rsgntnydygaielsepigntvgyfgysytts 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                               constituents in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is Bacillus licheniformis (BLC) RP-II protease variant (G55R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 vigsddrtrvtnttaypyraivhisssigsctgwmigpktvataghciydtssrsfagta
                                                                                                                                                                                                                                                                                                                         protein, their
Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 222;
                                                                                                                                                                                              detergent compositions, additives and cleaning compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus licheniformis RP-II protease variant (T15R).
                                                                                                                                                               Novel RP-II type protease and its variants, useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 412.5; DB 22;
Pred. No. 3.4e-25;
Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 srtncsgpcslavhtngvyggssynrgtrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers
Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                               Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.5%;
39.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE00036 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus licheniformis.
                                                                                                  2001-226680/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 84; Conserv
                                     Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 AA;
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FXY

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Residual protease II; RP-II; additive; cleaning composition; detergent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions -
                                                                                                                                                                                                                                             /note= "Wild type Ser substituted with Arg"
                                                      Bacillus licheniformis RP-II protease variant (S116R)
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             99DK-0001212:
                                                                                                                                                                                                                                                                                                                                                        31-AUG-2000; 2000WO-DK00476.
                   (first entry)
                                                                                                              mutant; mutein; variant.
                                                                                                                                             Bacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norregaard-madsen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVOZYMES AS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-226680/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 AA;
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                WO200116285-A2.
                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1999;
20-OCT-1999;
                                                                                                                                                                                                                                                                                                                 08-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase.
                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   especially towards
                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 slvgttvtisgypgdktagt----qwqhsgpiaisetyklqyamdtyggqsgspvfegss 176
                                                                                                                                                                                                                                                                                                                                    Novel RP-II type protease and its variants useful as constituents in detergent compositions, additives and cleaning compositions ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 vigsddrtrvtntraypyraivhisssigsctgwmigpktvataghciydtssgsfagta 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peroxidase.
The present sequence is Bacillus licheniformis (BLC) RP-II protease
variant (T15R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ
                                                                                                                                                                                                                                             Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 411.5; DB 22; Length 222;
Pred. No. 4e-25;
5; Mismatches 76; Indels 15;
/note= "Wild type Thr substituted with Arg"
                                                                                                                                                                                                                                           Rahbek Ostergaard P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 srtncsgpcslavhtngvyggssynrgtrit 207
                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                               99DK-0001212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.4%;
                                                                                                          31-AUG-2000; 2000WO-DK00476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                           Norregaard-madsen M,
                                                                                                                                                                                                        (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                               WPI; 2001-226680/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                              Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 AA;
                                    W0200116285-A2
                                                                                                                                                               20-OCT-1999;
                                                                                                                                               31-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84;
                                                                         08-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE00116
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Rahbek Ostergaard P, Voge Christensen CB;

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Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein [SEQ ID NO: 2] shown in page 101-102 of the specification (AAE000II). The specification also refers to following variants: (a) VIF, (b) D7G+T125S+E152G+M1821, (c) S119A+S144T+O157R+S1751, (d) H141A, (e) E152A+O122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), H1s residue in (d) and (f), Ser residues in (c) and (d), din residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.
                                                                                                                                                                                                                                                                         peroxidases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ 267
The present sequence is Bacillus licheniformis (BLC) RP-II protease variant (S116R).

The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amplases, peroxidase or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towar the action of proteolytic enzymes and improved resistance towards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 vigsddrtrvtnttaypyraivhisssigsctgwmigpktvataghciydtssgsfagta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.4%; Score 411.5; DB 22; 39.8%; Pred. No. 4e-25; tive 36; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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AAE00116 standard; Protein; 222 AA.

AAE00116;

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The patent discloses RP-II (Residual protease II) protein, their corresponding nucleic acid sequences and variants. RP-II protease is useful as a constituent in additives, detergent compositions and other cleaning compositions, optionally in combination with other enzymes such as proteases, lipases, cellulases, amylases, peroxidases or oxidases. The variants of RP-II have improved properties such as substrate specificities, catalytic rate, stability, especially towards the action of proteolytic enzymes and improved resistance towards peroxidase.
                                                                                                                                                                                                                                                                                                                           Residual protease II; RP-II; additive; cleaning composition; detergent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Bacillus licheniformis (BLC) RP-II protease variant (T128K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel RP-II type protease and its variants useful as constituents detergent compositions, additives and cleaning compositions \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rahbek Ostergaard P, Voge Christensen CB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Thr substituted with Lys"
                                                                                                                                                                                                                                                                                         Bacillus licheniformis RP-II protease variant (T128K).
                                                    268 Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                        177 srtncsgpcslavhtngvyggssynrgtrit 207
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                 AAE00118 standard; Protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 3; Page -; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99DK-0001212.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-2000; 2000WO-DK00476.
                                                                                                                                                                                                                                                         31-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus licheniformis. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norregaard-madsen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-226680/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flensted Lassen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200116285-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2001
                                                                                                                                                                                                                     AAE00118;
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                                                                                                                                               RESULT 1
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Note: This sequence is not shown in the specification but is derived from the mature B. licheniformis RPII protein [SEQ ID NO: 2] shown in page 101-102 of the specification (AAEDONIL). The specification also refers to following variants: (a) VIF, (b) D764T1255\*E1526+N1821, (c) S119A+5144T+Q157R+S1751, (d) H141A, (e) E152A+Q122R, (f) N182T+C185A, (g) E152A+V144L and (h) E104K+Q204R. However the positions of Val in (a) and (g), Asn residue in (b) and (f), Ser residues in (c), His residue in (d), Gln residue in (e) and (h) do not match with the B. licheniformis native wild type RPII protease sequence.

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Sequence

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208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ 267
                                                          89 VIGDDGRIKVINTRVAPYNSIAYITFGGSSCTGTLIAPNKILINGHCVYNTATRSYSAKG 148
                              Gaps
                                                                           149 SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-
                              15;
 Length 222;
26.4%; Score 411.5; DB 22; Length 39.8%; Pred. No. 4e-25; ive 36; Mismatches 76; Indels
                                                                                                                                                                                                                                        268 Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                    177 srtncsgpcslavhtngvyggssynrgtrit 207
                              Conservative
 Query Match
Best Local Similarity
                             84;
                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TERVFGKDORTVVNNILQRPYKQTVLLNMTFSNNRVYKGTGTMIGKDIVLTAAHNVYSKD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21311952; PubMed-11418146; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagal T., Lan J.-O., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
                                                     MAYIGDDGRIKVINTRVAPYNSIAYITFGGSSCT
                                                                                              GTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGYINTGA
                                                                                                                      241 REDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFINYAK
                                                                                                                                                                                                                              VLTSDY --- DMVTSDGKVISSADFHNDMKTPS-SFDKVDDLSSTIGEKVKPLTTYLKDFQ
                                                                  SQYDFAVIKTDTNIGNTVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.9%; Score 341; DB 16; Length 358; 32.6%; Pred. No. 7.2e-15; Live 51; Mismatches 111; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteome.
5AB5B04202583B08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus (strain Mu50).
Bacteria; Firmicutes; Bacillus/Clostridium group;
Maker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus/Staphylococcus group; Staphylococcus NCBI_TaxID=158878;
                                                                                                                                                                                                                                                                                                                                                               358
                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                     DKVDDLSSTIGEKVKPLTTYLKDFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lancet 357:1225-1240(2001).
EMBL; AP003365; BAB58758.1; -.
Hypothetical protein; Complete
SEQUENCE 358 AA; 41086 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL PROTEIN SAV2596.
                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 32.6% es 91; Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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01-DEC-2001 (
01-DEC-2001 (
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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Najmpo S., Sugimoto M., Tabata S.; Sugimoto M., Sagimoto M., Tabata S.; Sugimoto M., Sagimoto M., Sugimoto M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 VIGDDGRTKVTNTRVAPYNSIAYI-----TFGGSSCTGTLIAPNKILTNGHCVYNTATR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 VFGPDDREQVRNTKTYPFSAIGYLEAKSAKTGSYGSCSATLIGPRTVLTAAHCLYSHEDK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 SYSAKGSVYPGMNDSTAVN---GSANMTEFYVPSGYINTGASQY-----DFAVIKTDTN 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 DWLSEYLFVPGLNGSTADDAPFGAFTYESAYVLQGFIDNYQGYYGSVIPWDLGIITLKQD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 VGTNLGWLGYANYDDLGDFTANLVGYPGDKPMGT----MWKASCEVHAENIAPEYFQYDC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 IGNTVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAY--YTI
                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMC03769.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTFSGNSGSAML - - - - DQNQQIVGVHNAGYSNGTINGGPKATAAFVEFIN 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13BE653270E7CDD3 CRC64;
                                                                                                                                                                                                                                       01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                         277
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                                                                                                                                                                                                                                                                                                                                   GLUTAMYL ENDOPEPTIDASE (EC 3.4.21.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AP003001; BAB50229 1; -. InterPro; IPR00126; Ser_proteas_V8 InterPro; IPR001254; Trypsin.
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC; 1.
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Best Local Similarity 30.3%;
Matches 70; Conservative
                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=381;
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                                                                                                                     RESULT
Q98GI7
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SAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFINY 298

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RSIRQVTNLT-GTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSG

TRSYSAKGSVYPGMNDSTAVNGSANWTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGY 127 DKGWAKKIDVYAGVNGQTYTIGKAFSHKFFVSKTWINNAPTKEDIAIIKLNSNLGNKTGY

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PROSITE; PS00673; V8_SER; 1.
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                                              Analyser F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barloy-Hubler F., Finan T.M., Long S.R., Puehler A., Boistard P., Bothe G., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., A., Boutry M., Bowser L., Burmester J., Cadieu E., Capela D., Chain P., A. Cowle A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., A. Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., A. Harandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Rahn D., Rann M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., A. Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., A., Porheelter F.J., Weidher S., Wells D.H., Wong K., Yeh K.-C., Batut J.; A. The composite genome of the legume symbiont Sinorhizobium mellioti."; EMBL, AL591793; CAC47733.1; -- Complete proteome.

Complete proteome.

SeQUENCE 639 AA, 69813 MW; 320E86D3050DFB67 CRC64;
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6
                                                                                                                                                                                                                                                                                                                                                 89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSS-----CTGTLIAPNKILTNGHCVYN-TATR 142
                                                                                                                                                                                                                                                                                                                                                                                                       143 SYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQ----YDFAVIKTDTNIGNTV 198
                                                                                                                                                                                                                                                                                                                                                                                                                        472 EPFONFRIIPGRNLGAAPFGRCLGVGASVLAGWTASATTDQSRYYDLGAIKLNCNIGDTT 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GYRSIRQVTNLTGTTIKISGYPGDKMRSTGK--VSQ-----WEMSGPVTREDTNLAYYT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FYQ 580
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                      31;
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"Characterization of the gene encoding glutamyl endopeptidase Staphylococcus warneri M.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293885; CAC06168.1;
                                                                                                                                                                                                                                                                                          DB 16; Length 639;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532 GWLGVRTIGNDEAIDTVVOGYAADR-APTGROWVSEDKLRILWQLKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                         14.6%; Score 227.5; DB 1 30.3%; Pred. No. 3.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmloutes; Bacillus/Clostridium grc
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 AA
                                                                                                                                                                                                                                                                                                                    31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 IDTFSGNSGSAML -- DQNQQIVGVHNAG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                       MEDLINE-21368234; PubMed-11474104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, GLUTAMYL ENDOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                      63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                         Local Similarity
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             FROM N.A
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Matches
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Q9FBG1
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16;
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MEDLINE-21311952; PubMed-11418146;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Gui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ul Y.,

Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,

Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                      60 FDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITF----G 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 INTGASQY - - - - DFAVIK - - - - - TDTNIGNTVGYRSIRQVTNLT - GTTIKISGYPGDKMR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 AVIKTDTNIGNTVGYRSIRQVTNLT-GTTIKISGYPGDKMRSTGKVSOWEMSGPVTREDT 244
                                                                                                                                                                                                                                                                       2 KVKFFTASSLLIATLISATLINPAHAETTS-STDNHQOTTQS-------QQQKTP-- 48
                                                                                                                                                                                                                                3 KVKKLIPSLLVFGALSVPSF---AHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSS 59
                                                                                                                                                                                                                                                                                                                                                                                                            49 --KIDK-----GNNVKPVE---KKERANVILPNNDRHQINDTTLGHYAPVTFVQVQSNEG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 STGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGG
                                                                                                                                                                         62;
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                                                                                                                Length 316;
                                                                                                                                                                         Indels
                              4E997A5A111DDB40 CRC64;
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Last annotation update)
                                                                                                             Score 214; 'DB 2; I
Pred. No. 1.3e-06;
I; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 AA
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InterPro; IPR000126; Ser_proteas_V8.
PRINTS; PR00839; V8PROTEASE.
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                                                                                                                                                                      54;
Hydrolase; Serine protease.
SEQUENCE 316 AA; 34296 MW;
                                                                                                             13.7%;
25.0%;
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                                                                                                                                                                         Conservative
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                                                                                                             Query Match
Best Local Similarity
Matches 77; Conserv
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Matches 46; Conserv
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SEQUENCE 188 AA;
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SPECIES—S. aureus (strain N315), and.S. aureus (strain Mu50);
MEDLINE—21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kalto C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 VDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITF----GGSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 CTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYP-GMNDSTAVNGSANMTEFYVPSGYIN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 TGASQYDFAVIKTDTNIGN------TVGYRSIRQVTNLTGTTIKISGYPGDKMRST 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KVSSLFVATLTTATLVSSPAANALS-----SKAMDNHPQQTQSSKQQ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSFDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hydrolase; Protease; Serine protease.
SEQUENCE 342 AA; 36977 MW; 5AEF42DCE01C4B24 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SERINE PROTEASE, V8 PROTEASE, GLUTAMYL ENDOPEPTIDASE.
STAPA OR SA0901 OR SAV1048.
Staphylococcus aureus (strain N315), and
Staphylococcus aureus (strain M50).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lancet 357:1225-1240(2001).
-!- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.2%; Score 189.5; DB 16; Best Local Similarity 24.2%; Pred. No. 5.7e-05; Matches 74; Conservative 45; Mismatches 126;
                                                                                                                                                  Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBL_TaxID=158879, 158878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 AA.
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01-JUN-2001 (TrEMBLrel. 17, Created)
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InterPro; IPR001254; Trypsin.
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PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
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EMBL; AP003361; BAB57210.1;
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Q9AJX0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 IQK-----GGNLKPLE---QRERANVILPNNDRHQITDTTNGHYAPVTYIQVEAPTGTFI 103
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*Purification, characterization and gene cloning of a novel glutamic acid-specific endopeptidase from staphylococcus aureus atcc 12600.*;
*EMBL; D00730; BAA00630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
      55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 KVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSFDK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQTD------K00TP----K51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AIIKLNSNLGNKTGYLTLN--THISKGENIEISGFPGDKSDN----RQYKGKGKLESFDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                      01-NOV.1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GLUTAMIC ACID SPECIFIC PROTEASE PREPROPEPTIDE (EC 3.4.21.19).
Staphylococcus aureus.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
NCBI_TaxID=1280;

    s) Score 192.5; DB 2; Length 357;
    pred. No. 3.8e-05;
    Mismatches 127; Indels 73

                                                245 NLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFINY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
58AA9A4E371E2577 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 AA.
                                                                                                                                                                                                  Ž
                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00126; Ser_proteas_V8.
InterPro; IRR001254; Trypsin.
Pfam; PR00189; trypsin; IPRINTS; PR00839; V8PROTEASE.
PROSITE; PS00240; TRYPSIN_DOM; I.
PROSITE; PS00672; V8 HIS; I.
PROSITE; PS00673; V8 HIS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s, Serine protease.
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VEFINYA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 -- AVFINENVRNFLKQNIEDINFA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38651 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.3%;
23.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 23.8%
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 ATAAF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099V45
099V45;
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RESULT 8 099V45 ID 09 AC, 09

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74 CITSPIRORLGLPNLAVRIRVTPGRASRDARPFGWQWAKQWHVNPPYRRRPSGLHDVGLI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 KTDTNIGNTVGYRSI-----RQVTNLTGT-TIKISGYPGDKMRSTGKVSQWEMSGPVTRE 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 CVYNTATR----SYSAKGSVYPGMNDSTA-VNGSANMTEFYVPSGYINTGASQYDFAVI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 LKDFQTKVVIG-DDGRTKVTNTRVAPYNSIAYI--TFGG---SSCTGTLIAPNKILTNGH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 LADEADYAVVGPTDGRARVTHTNRFPHSAVCHIERDFGDGRMTGCTAFLISPTRLLTAAH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 DINLAYYIIDIFSGNSGSAMLDQNQQ----IVGVHNAG---YSNGTIN---GGPKATA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-OG1-10;
Su Y.A., Clewell D.B.;
A gene (sprE) downstream of gelE of Enterococcus faecalis OG1-10
resembles serine proteinase determinant of Staphylococcus aureus
strain VB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 187.5; DB 16; Length
Pred. No. 5.8e-05;
2; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                    271 AA; 30385 MW; 37659307C63D0D9C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31063 MW; D4F0312BEE778415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
STAPHYLOCOCCAL SERINE PROTEINASE HOMOLOGUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.5%; Score 179.5; DB 2; 25.5%; Pred. No. 0.00021; ive 40; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR00126; Ser_proteas_V8.
InterPro; IPR001254; Trypsin.
PRINTS; PR00839; V8PROTEASE.
PROSITE: PS50240; TRYPSIN.DOM: 1.
PROSITE; PS00673; V8_HIS; 1.
PROSITE; PS00673; V8_ERE; UNKNOWN_1.
HVATClase; Serine protease.
SEQUENCE 284 AA, 31063 MW: D4F0312)
                             DNA Res. 7:331-338(2000).
EMBL; AP003010; BAB53084.1; -.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Trypsin.
Pf00089; trypsin; 1.
                                                                                                                                                                                                                 PRINTS; PRO0722; CHYMOTRYPSIN. PRINTS; PR00839; V8PROTEASE. SMART; SM00020; Tryp_SPC; 1. PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%;
27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Conservative
Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterococcus
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   RATE DAY A MARKET SOLVER A MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 VVIGDDGRTKVTNTRVAPYNSIAYITF----GGSSCTGTLIAPNKILTNGHCVYNTATRS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 YSAKG----SVYP-GMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTN---- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 HIGOVVKPATISSNTDTRINENITVTGYPGDKPLAT----MWESVGKVVYIGGEELRYDL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 NGAKGNPRNISVHPSAKNENDYPNGKFVGQEIIPYPG-----NSDLAILRVSPNEHNQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 -IGNTVGYRSIRQVTNL-TGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 VILPNNNRHQIFNTTQGHYDAVSFIYIPIDGGYMSGSGVVVGENEILTNKHVV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteòbacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                          "Staphylococcus epidermidis extracellular serine proteinase.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ305145; CAC27157.1;
HSSP; P09331; 1EXF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 EXTRACELLULAR SERINE PROTEINASE. 23667 MW; FB9B886D453B8BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Indels
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXTRACELLULAR SERINE PROTEINASE PRECURSOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
GLUTAMIC ACID SPECIFIC ENDOPEPTIDASE.
MLL6878.
                                                                                                                           Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.1%; Score 189; DB 2; Best Local Similarity 28.4%; Pred. No. 3.6e-05; Matches 59; Conservative 32; Mismatches 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 DTFSGNSGSAMLDQNQQIVGVHNAGYSN 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 STVGGNSGSPVFNGKNQVIGIHYGGVDN 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000126; Ser_proteas_V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001254; Trypsin.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS0040; TRYPSIN_DOM; 1.
PROSITE; PS00673; V8_EER; 1.
Hydrolase; Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21082930; PubMed-11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        217 AA;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-MAFF303099;
                                                                                                                                                                                                                           NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                           STRAIN-6746;
                                                                                                                                                                                                                                                                                                                                                         Dubin G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SQYDFAVIKTDTNIGNTVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 TISGYPGEKNH-----TQWSHENDLFTSNFTDLENPLLFYDIDTTGGQSGSPIYNAQFEV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 ----TGEVVGTNTIVTNNHVAESFKNAKVLNPNAKDDAWFYPGRDGSATPFGKFKVIDVA 141
                                                                                                                                                                                                                                                                                                    78 TTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 LSANAEEYIVPAESHSRQ-KRSLLDPEDRRQEVADTTEAPFASIGRIISPASKPGYISLG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed S.B., Wesson C.A., Liou L.E., Trumble W.R., Schlievert P.M., Bohach G.A., Bayles K.W.;
*Molecular Characterization of a Novel Staphylococcus aureus Serine
                                                                                                                                                                                                                                                           170 YVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIR-------QVTNLTGTTI
                                                                                                                                                                                                                                                                                                                                                                                         215 KISGYPGDKMRSTGKVSQWE-----MSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQI
                                                                                                                             116 GSSCTGTLIAPNKILTNGHCV---YNTATRSYSAKGSV--YPGMNDSTAVNGSANMTEF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 174.5; DB 2; Length 240; 28.4%; Pred, No. 0.00036; tive 31; Mismatches 78% Indels 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease Operon.;
Infect. Immun. 69:1521-1527(2001).
EMBL; AF271715; AAF97926.1;
MEROPS; S01.282;
InterPro; IPR00126; Ser_proteas_V8.
InterPro; IPR00126; AT TYPS1N.
InterPro; IPR00189; V8PROTEASE.
R PROSITE; PS50240; TRYPS1N DOM; 1.
PROSITE; PS06722; V8—HIS! 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 240 AA; 26096 MW; 00A3349FIFE5D52E CRC64;
LSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSI - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 REDINLAYYIDTFSGNSGSAMLDQNQQIVGVHNA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 VGVHNAGYSNGTINGGPKATAAFVEFI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VGVHSNGGIKQTGNHGQRLNEVNYNFI 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-8325-4;
MEDLINE-21116966; PubMed-11179322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, CTEMBLrel. 15, ICTEMBLrel. 19, ICTEMBLREL. 19,
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Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel
01-OCT-2000 (TrEMBLrel
01-DEC-2001 (TrEMBLrel
SERINE PROTEASE SPLB.
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SPECIES-S. aureus (strain N315), and S. aureus (strain Mu50);
MEDLINE-21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Magai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Puruya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SQYDFAVIKTDTNIGNTVGYRSIRQVTNLFGTTIKISGYPGDKMRSTGKVSQWEMSGPVT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 N-----TATRS-----YSAKGSV-YPGMNDSTAVNGSANMTEFYVPSGY-INTGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 TPFKYAA-----GAKAGER------IKVIGYPHP---YKNKYVLYESTGPVM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 TIYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NYKVGDRITAHPNSDKGNGGIYSIKKIINYPGKEDVSVIQVEERAIE-RGPKGFNFNDNV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 TILVEEVQ-QTAKAENNVTKIQDTNIFPYTGV--VAF--KSATGFVVGKNTILTNKHVSK 78
                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S.aureus; STRAIN-FDA #485 (ABD ENT+);
Rieneck K., Renneberg J., Gutschik E., Diamant M., Svenson M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
11.1%; Score 173.5; DB 16; Length 240;
Best Local Similarity 27.9%; Pred. No. 0.00042;
Matches 60; Conservative 32; Mismatches 78; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome; Hydrolase; Protease, Serine protease.
SEQUENCE 240 AA; 26140 MM; 45EF0B5A51E06DA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY. EMBL; U60589; AAB03613.1; -. EMBL; AP003135; BAB42898.1; -. EMBL; AP003135; BAB57974.1; -. MEROPS; SOL.282; -. InterPro; IPR00126; Ser_proteas_V8.
                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                   Staphylococcus aureus (strain MuSO).
Bacteria: Firmicutes; Bacillus/Clostridium greaclilus/Staphylococcus group; Staphylococcus NCBI_TaxID-1280, 158879, 1588788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 SVEGSSIVYSAHTESGNSGSPVLNSNNELVGIHFA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 REDINLAYYIIDTFSGNSGSAMLDQNQQIVGVHNA 275
176 SVEGSSIVYSAHTESGNSGSPVLNSNNELVGIHFA 210
                                                                                                  $
                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain N315), and
                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-DEC-2001 (TrEMBLrel. 19, Last ann NOVEL ANTIGEN (SERINE PROTEASE SPLB) SPLB OR SA1630 OR SAV1812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00672; V8_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lancet 357:1225-1240(2001).
                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bendtzen K.;
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                                                                                                  053781
                                                          RESULT 13
053781
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Gaps

46;

Length 239; 88; Indels

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96 TKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCV--YNTATR----- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                               143 --SYSAKG-SVYPGMNDSTAVNGSANMTEFYVPSGY-INTGASQYDFAVIKTDTNIGNTV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 GYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 -------KIKVIGYP---LPAQNSFKQFESTGTIKRINILNFDAYIEPGNS 193
"Molecular Characterization of a Novel Staphylococcus aureus Serine
                                                                                                                                                                                                                                                                                                                                                                                                              41 TQVKDTNIFPYNGV--VSF--KDATGFVIGKNTIITNKHVSKDYKVGDRITAHPNGDKGN
                                                                                                                                                                                                                                                  BA797E14786B2DBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 GSPVLNSNNEVIGVYGGIGKIGSEYNGAVYFTPQIKDFI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 GSAMLDQNQQIVGVHNAGYS--NGTINGGPKATAAFVEFI 296
                                                                                                                                                                                                                                                                                                  Query Match 10.0%; Score 156; DB 2; Best Local Similarity 25.9%; Pred. No. 0.0058; Matches 57; Conservative 29; Mismatches 88.
              Protease Operon.";
Infect. Immun. 69:1521-1527(2001).
EMBL, AF771715; AAF97927.1; -
MEROPS; SO1.283; -
InterPro; IPR001940; Protease2C.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Trypsin.
Pfam: PF00089; trypsin: 1.
PRINTS; PR00834; PROTEASESC.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS50240; TRYPSIN.DOM; 1.
PROSITE; PS50240; TRYPSIN.DOM; 1.
Hydrolase; Protease.
SEQUENCE 239 AA; 26098 MM; BA797E14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 VTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNI----GNTVGYRSIRQVTN--LT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 GTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=8325-4;
MEDLINE=21116966; PubMed=11179322;
Reed S.B., Wesson C.A., Liou L.E., Trumble W.R., Schlievert P.M.,
Bohach G.A., Bayles K.W.;
                                                                                                                                                                                                                                                                                STRAIN-FRI 326;
Nair S.P., Williams R.J.;
Cloning and expression of two genes from a novel Staphylococcus aureus operon encoding serine protease like exproteins.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: APG95601; AAG02239.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 10.3%; Score 161; DB 2; Length 238; Best Local Similarity 28.7%; Pred. No. 0.0027; Matches 58; Conservative 22; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Protease; Serine protease.
SEQUENCE 238 AA; 25724 MW; 4A94E5B0F1C437B7 CRC64;
                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SERINE PROTEASE-LIKE EXOPROTEIN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacieria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus. NCBL_TaxID=1280;
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                                                   238 AA.
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InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00672; V8_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 GVHFGG--NGPANKSTKGYGVY 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 GVHNAGYSNGTINGGPKATAAF 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                   PRELIMINARY;
                                                                                                                                                                            Staphylococcus aureus.
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SEQUENCE FROM N.A.
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                                                  Q9FD07
              RESULT 14
Q9FD07
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2002, 18:40:36;		
2002,		
June 21, 2		
Run on:		

	US-09-652-743A-12 1559 1 MKKVKKLIPSLLVFG	43A-12		MKKVKKLIPSLLVFGALSVPNGGPKATAAFVEFINYAKAQ 302
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283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 ring table: ...arched: 283138 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR\_71:\* 1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ه ،	metalloproteinase	hypothetical prote	glutamic acid-spec	glutamyl endopepti	hypothetical prote	probable pepetidas	serine proteinase	serine proteinase	choline binding pr	probable serine pr	epidermolytic toxi	hypothetical prote	Putative protease	choline binding pr	serine proteinase	serine proteinase	serine protieinase	serine proteinase	probable secreted	hypothetical prote	epidermolytic toxi	hypothetical prote	trypsin-like prote	outer membrane pro	hypothetical prote	probable serine pr	cell wall-binding	trypsin-like prote
														1	٠.	-														
SUMMARIES		34	22	65	28	SK	73	82	04	67	15	15	EA	65	15	4.5	67	99	67	67	82	99	EB	69	20	40	22	68	25	3.Y
S	ΙΩ	A4513	A35122	E90063	S21758	PRSASK	G89873	AH0282	\$25140	C89967	E97915	B82415	PRSAEA	E85765	H64915	C950	B89967	<b>Н89966</b>	D89967	A89967	AE0682	990060	PRSAEB	T33369	JC4170	JC1340	A69222	H70789	B69825	TRWV3Y
	DB	7	~	~	7	-	7	~	7	~	7	~	<del>, ,</del>	7	7	7	7	7	~	7	~	7	Н	~	7	~	7	7	~	-
	Query Match Length	316	313	188	357	336	342	278	284	240	218	330	280	273	273	285	239	239	235	239	273	168	277	1275	272	1651	869	397	488	254
ď	Query Match	27.0	18.0	13.0		12.2	_	٦		11.1	10.9	10.0	10.0	6.6		•	9.6	9.1	8 6.8		œ	•		•			8.0	7.8	7.7	7.7
	Score	٠.	280.5	202.5		189.5	189.5	182.5	179.5	173.5	170.5	156	155.5	'n	153.5	153.5	150	141.5	139.5	137.5	35	133.5	133	130	128.5	125	124	121	120.5	120
	Result No.	C	ار	m (	7	พ	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

probable PPE prote	serine proteinase	toain-like outer m	hypothetical prote	MG321 homolog H08_	periplasmic L-aspa	periplasmic L-aspa	alpha-glucosidase	probable membrane-	probable secreted	hypothetical prote	hypothetical prote	_	hypothetical prote
A70762 S75138	A69643 B82414	B64635	н90916	S73708	A98108	D85953	F97177	F87196	T34585	S37842.	T16509	AH2493	F90073
2.0	010	2	7	~	7	7	7	7	~	7	~	7	7
678	449	2529	174	591	348	348	1217	401	411	619	786	3083	2271
7.6	7.5	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2
119	116.5	114	113.5	113	112.5	112.5	112.5	112	112	112	112	112	111.5
30	32	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  A45134 endopeptidase (EC 3.4), glutamate-specific - Bacillus licheniformis C;Species: Bacillus licheniformis C;Species: Bacillus licheniformis C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C;Accession: A45134; S23078 R;Rakudo, S., Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, I. R;Rakudo, S., Kikuchi, N.; Kitadokoro, K.; Fujiwara, T.; Nakamura, E.; Okamoto, I. A;TILTE-reutfication, characterization, cloning, and expression of a glutamic ac A;Reference number: A45134; MUID:93054737 A;Reference number: A45134 A;Reference number: A51134 A;Reference number: A51134 A;Reference number: A5104 A;Status: preliminary A;Molecule type: DNA	A; Residues: 1.316 <kak> A; Cassing terrores: CB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d1001415; PID:g5 A; Cass = references: CB:D10060; NID:g216263; PIDN:BAA00949.1; PID:d1001415; PID:g5 A; Experimental source: ATCC 14580 A; Experimental source: ATCC 14580 A; Note: sequence extracted from NCBI backbone (NCBIN:118784, NCBIP:118785) B; Svendsen, I.; Breddam, K. Eur. J. Biochem. 204, 165-171, 1992 A; Title: Isolation and amino acid sequence of a glutamic acid specific endopeptic A; Reference number: S23078; MUID:92155199 A; Title: Isolation and amino acid sequence of a glutamic acid specific endopeptic A; Reference number: S23078 A; Article: Isolation and amino acid sequence of a glutamic acid specific endopeptic A; Reference number: S23078 A; Reference number: S23078 A; Residues: 95-316 <sve> C; Reywords: hydrolase</sve></kak>	Duery Match  27.0%; Score 420.5; DB 2; Length 316;  Best Local Similarity 33.0%; Pred. No. 2.18-22;  Matches 101; Conservative 55; Mismatches 121; Indels 29; Gaps 10;  5 KKLIPSLLVFGALSVPSFAHAASDSVLTSDYDWTSDCVVISSADFHNDMKT 56  11: 1: 1: 1: 1	57PSSFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYIT 113 :	114 FGGSSCTGTLIAPNKILINGHCVYNTATRSYSAKGSVYPGWNDSTAVNGSANMTEFYVPS 173      :       :     :  :   :        ::    121 SSIGSCTGWMIGPKTVATAGHCIYDTSSGSFAGTATVSPGRNGTSYPYGSVKSTRYFIPS 180	174 GYINTGASQYDFAVIKTDTNIGNTYGYRSIRQYT-NLJGTTIKISGYPGDKMRSTGKVSQ 232 	233 WEMSGPUTREDTNLAYYIDTFSGNSGSAMLDQNQQIVGVHNAG-YSNGTIN 283 
RESULT A45134 endopepti C. Speciec C. Jaccessi C. Accessi R. Kakudo A. Hiller A. Referer A. Referer A. Referer A. Accessi A. Anolecul	A, Residue A, Cross - 1 A, Cross - 1 A, Note: s, A, Note: s, B, Svendse Bur. J. B, Tille: A, Referer A, Referer A, Access: A, Molecus A, Residue C, Keyword	Query Match Best Local Matches 10 Qy 5 KKL Db 4 KKS	Qy 57 Db 62	Qy 1114 Db 121	Qy 174 Db 181	Qy 233
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C; Accession: $21758
R; Yoshikawa, K.; Tsuzuki, H.; Fujiwara, T.; Nakamura, E.; Iwamoto, H.; Matsumoto, Biochim. Biophys. Acta 1121, 221-228, 1992
A; Title: Purification, characterization and gene cloning of a novel glutamic acid-A; Reference number: $21758; MUID: 92287954
A; Accession: $21758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000018; PID:g13702546; PIDN:BAB43687.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: SA2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Culma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekin C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SA2382 [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E90065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Staphylococcus aureus
C.Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
                                                                                                                                                    186 AVIKTDTNIGNTVGYRSIRQVTNLT-GTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 KVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSFDK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:D00730; NID:g216970; PIDN:BAA00630.1; PID:g216971
C;Superfamily: staphylococcal serine proteinase
       170 YPYGTYSCTMFYSVKGWTESKDTNYDYGAIKLNGSPGNTVGWYGYRTTNSSSPVGLSSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYT1DTFSGNSGSAML----DQNQQ1VGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----KQQTP----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 NLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFINY 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KVSSLFVATLTTATLVSSPAANALSSKAMDNHPQQTQTD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.3%; Score 192.5; DB 2;
ilarity 23.8%; Pred. No. 2.9e-06;
Conservative 47; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.0%; Score 202.5; DB 2
40.4%; Pred. No. 2.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
                                                                                                                                                                                                                                                                                           286 HTNGGS--SYNLGTRVTNDVFNNIQY 309
                                                                                                                                                                                                                                            273 HNAGYSNGTINGGPKATAAFVEFINY 298
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 46; Conserv
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A; Residues: 1-188 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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A; Accession: 140010
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-60,65,'L',67,'S',69,'AQA' <RES>
A; Crossreferences: GBM22916; NID: 9143701; PIDN: AAA22832.1; PID: 9143702
A; Residues: 1-60,65,'L',67,'S',69,'AQA' <RES>
A; Crossreferences: GBM22916; NID: 9143701; PIDN: AAA22832.1; PID: 9143702
B; Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A. M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A; Effilich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, R.; Lapidus, A.; Latinois,
A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
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T.; Whiters, P.; Whather, A.; Tamaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Vohlyama,
A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A; Ritle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Archererere number: A69580; MUID: 98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A69660
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-313 < KUN>
A; Cross-references: 6B: Z99105; GB: AL009126; NID: 92632457; PIDN: CAB12018.1; PID: e1182176;
A-Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1th, H.; de Jong, A.; Bron, S.; Venema, G.
70, 351-351, 1988
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                                                                                                                                                                                                                                                                                                                                                                                         .;
O
                                                                                                                                                                                                metalloproteinase (EC 3.4...) mpr precursor, extracellular - Bacillus subtilis metalloproteinase (EC 3.4...) mpr precursor, extracellular - Bacillus subtilis C;Species: Bacillus subtilis C;Species: Bacillus subtilis C;Cate: 27-uul-1990 #text_change 15-oct-1999 C;Accession: A35122; 140010; A66660 A.; Sullivan, B.J.; Theriault, K.A.; Ally, D B; Bacteriol. 172, 1034-1029, 1990 A.; Bacteriol. 172, 1034-1029, 1990 A.; Sullivan, B.J.; Theriault, K.A.; Ally, D A;Reference number: A35122; MUD::90130256 A;Accession: A35122 A;Status: preliminary A;Accession: A35122 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-313 < CLO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 AVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVTNLT--GTTIKI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSFDKVDDLSST---IGEKVKPL----TTYLKDFQT---KVVIGDDGRTKVTNTRVAPYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KLVPRFRKQWFAYLTVLCLALAAAVSFGVPAKAAENPQTSVSNTGK---EAD----ATK 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 KLIPSLLV--FGALSVPSFAHAASDS-----VLTSDYDMVTSDGKVISSADFHNDMKTP 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ve: mpr
ywords: hydrolase
284 GGPKAT 289
                                           | : |
RGTRIT 301
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Best Local S
Matches 96
                                                                    296
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ROTTO MANAGEMENT CONTRACTOR CONTR

Oy 63 VDDLSSTIGEKVRPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSS 118  1	Db 159EGDLAIVKFSPNEONKHIGEVVKPATMSNNAETOVNONITVTGYFGDKPVAT 210  Oy 228 GKVSQWEMSGPVTREDTNLAYTIDTFSGNSGSAMLDQNOQIVGVHNAGYSNGTINGGPK 287  Db 211MMESKGKTTYLKGEAMQYDLSTTGGNSGSPYFNEKNEVIGIHWGGVPN-EFNG 262  Oy 288 ATAAFV 293  Oy 288 ATAAFV 293     :
PRSASK glutamyl endopeptidase (EC 3.4.21.19) precursor - Staphylococcus aureus N.Alternate names: staphylococcal N.Alternate names: staphylococcus N.Alternate names: staphylococcus C.Secles: Staphylococcus aureus C.Secles: Staphylococcus aureus C.Secles: Staphylococcus aureus C.Secssion: A26812; A00966 R.Carmona, C.; Gray, G.L. Nucleic Acids Res. 15, 6757, 1987 A.Title: Nucleotide sequence of the serine protease gene of Staphylococcus aureus, strain A.Reference number: A26812; MUID:87316953	Lancet 357, 1225-1240, 2001 A.Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A.Reference number: A89758; MUID:21311952; PMID:11418146 A.Accession: G89873 A.Accession: G89873 A.Status: prefaliminary A.Molecule type: DNA A.Residues: 1-342 <kur> A.Residues: 1-342 <kur> A.Residues: 1-342 <kur> A.Steprimental source: strain N315 C.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetics: A.Genetimily: staphylococcal serine proteinase</kur></kur></kur>
	Query Best Match
A; Residues: 69-108;110-124;126-144, 'D',146-192, 'T',194-228, 'N',230-258, 'Q',260, 'D',262-2 A; Residues: 59-108;110-124;126-144, 'D',146-192, 'T',194-228, 'N',230-258, 'Q',260, 'D',262-2 A; Experimental source: strain v8 C:Comment: This extracellular proteolytic enzyme preferentially cleaves the peptide bond nument: This enzyme may be distantly related to the trypsin-type serine proteinases, perfamily: staphylococcal serine proteinase .eywords: hydrolase; serine proteinase F:69-336/Product: staphylococcal serine proteinase #status experimental <act> F:119,161/Active site: His, Asp #status predicted F:237/Active site: Ser #status experimental</act>	OY 63 YDDLSSTIGEKYRPLTTYLDEGTKVYICDOGRAFVTNINVAPNAINTITFGGSS 118    :     :     :
Query Match         12.2%;         Score 189.5;         DB 1;         Length 336;           Best Local Similarity 24.2%;         Pred. No. 4.3e-06;         Matches 74;         Conservative 45;         Mismatches 146;         Indels 61;         Gaps 12;           Qy 3 KVKKIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGVLSSADFHNDMKTPSSFDK 62         1   1   1   1   1   1   1   1   1   1	Oy 228 GKVSOWEMSGPVTREDTNLAYYIDTFSGNSGSAMLDONOOIVGVHNAGYSNGTINGGPK 287
Oy 63 VDDLSSTIGEKVRPLTTYLKDFOTKVVICDDGRTKVTNTRVAPYNSIAXITFGGSS 118	RESULT 7 AH0282 probable pepetidase YPO2319 [imported] - Yersinia pestis (strain CO92). C;Species: Yersinia pestis C;Date: 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: AH0282 C;Accession: AH0282 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentic deno-Tarkaga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.W.; Davis, P.; Dougi il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Br Nature 413, 523-527, 2001

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KVTNTRVAPYNSIA-----YITFGGSSCTG----TLIAPNKILTNGHCVYNTATRSYSA 146
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Best Local Similarity 27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 60; Conserv
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A: Residues: 1-218 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: cbpG-truncation
                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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S25140
Serine proteinase homolog - Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Species: Enterococcus faecalis
C; Species: C; Accession: S25140
R; Su, Y.A.; Clewell, D.B.
Submitted to the EMBL Data Library, June 1992
A; Description: A gene (sprE) downstream of gelE of Enterococcus faecalis OGI-10 resemble
A; Reference number: S25140
A; Reference number: S25140
A; References: S25140
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-284 <SUY>
A; Residues: 1-284 <SUY>
A; Cross-references: EMBL: Z12296; NID: 943337; PIDN: CAA78168.1; PID: 943338
C; Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                        11;
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                                    A; Accession: AH0282
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-278 - KUR>
A; Cross-references: GB:AL590842; PIDN:CAC91124.1; PID:g15980316; GSPDB:GN00175
C; Genetics:
A; Gene: YP02319
:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                               56 TPSSFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYI-TF 114
                                                                                                                                                                                                                                                                                                                                                                                               115 GGSSCTGTLIAPNKILTNGHCVYN-----TATRSYSAKGSVYPGMND-STAVNGSAN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                      SGNPCTATLISPRLVLTAGHCVLTPPGNIDQAVALRFISDKGHWKYQITDLKTRVDAKLG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MTEFYVPSGY1-NTGASQYDFAVIKTDTNIG------NTVGYRSIRQVTNLTGTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSI------AYITFG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GSSCTGTLIAPNKILTNGHCV---YNTATRSYSAKGSV--YPGMNDSTAVNGSANMTEF- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 ----TGFVVGINIIVTNNHVAESFKNAKVLNPNAKDDAMFYPGRDGSAIPFGKFKVIDVA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- QVTNLTGTTI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |: | : | : | 142 FSPNA------DIAVV------TVGKQNDRPDGPELGEILTPFVLKKFESSDTHV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                      17 TAFALDKPDGSNS-----IED-QTALFFGKDDRTAVTNSRQWPWEAIGQVETA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSANAEEYIVPAESHSRQ-KRSLLDPEDRRQEVADTTEAPFASIGRIISPASKPGYISLG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 IKISGYPGDKMRSTGK-----VSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQN 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 KISGYPGDKMRSTGKVSQWE-----MSGPVTREDINLAYYTIDIFSGNSGSAMLDQNQQI
                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
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                                                                                                                                                                                                                          Length 278;
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                          11.7%; Score 182.5; DB 2; 28.6%; Pred. No. 1e-05; Live 30; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96;
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25.5%; Pred. No. 1.7e-05;
ive 40; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 YVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 VGVHNAGYSNGTINGGPKATAAFVEFI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 VCVHSNGGIKQTGNHGQRLNEVNYNFI 266
                                                                                                                                                                                                                                                                      68; Conservative
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Best Local Similarity
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C;Species: Strepfococus pneumoniae
C;Species: Sgrib Baserocus plants: Sgrib Baserocus Britania Br
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A;Residues: 1-240 <KUR>
A;Cross-references: GB:BA000018; PID:g13701605; PIDN:BAB42898.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                    Cincession: C89967

Rikuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekin Ma, A.; Hizamatsu, K.
Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146
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serine proteinase SplB [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQYDFAVIKTDTNIGNTVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-----TATRS-----YSAKGSV-YPGMNDSTAVNGSANMTEFYVPSGY-INTGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 173.5; DB 2;
; Pred. No. 3.7e-05;
32; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 SVEGSSIVYSAHTESGNSGSPVLNSNNELVGIHFA 210
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27.9%;
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8

25; Gaps

Indels

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A;Experimental source: strain 2M
A;Note: the authors translated the codon ATT for residue 3 as Asn, CAA for residu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coding for staphylococcal exfoliative tox
                                                                                                                                                                                                                                                             Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYI-TFGGSSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSGYINTG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 ASQYDFAVI -- KTDTN---IGNTVGYRSIRQVTNL-TGTTIKISGYPGDKMRSTGKVSQW 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 EMSG-PVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSN----GTINGGPKA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KKVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMV-TSDGKVISSADFHNDMKTPSSF 60
                                                     A; Experimental source: strain UT0002 A; PIDN:AAA26625.1; PID:g153006 A; AAcession: C26680
                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB:M17357; NID:g153007; PIDN:AAA26626.1; PID:g153008
A.Experimental source: strain TC16
R.Balley, C.J.; Smith, T.P.
Biochem. J. 269, 535-537, 1990
Biochem. J. 269, 535-537, 1990
A.FILLE: The reactive serine residue of epidermolytic toxin A.
A.Reference number: S11541; MUID:90351379
A.Accession: S11541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGVDLALIRLKPDQNGVSLGDKISPAKIGTSNDLKDGDKLELIGYPFDH-----KVNQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DRQKYPYNTIGNVFVKGQTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                               A.Wolecule type: protein
A.Molecule type: protein
A.Mote: the carboxyl-terminal residue of the mature protein is Lys
                                                                                                                                                                                                                R;O'Toole, P.W.; Foster, T.J.
Sacteriol. 169, 3910-3915, 1987
A;Title: Nucleotide sequence of the epidermolytic toxin A gene of A;Reference number: A26679; MUID:87307960
A;Accession: A26679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: scalded skin syndrome; toxin
F;1-38/Domain: signal sequence #status predicted <SIG>
F;39-280/Product: epidermolytic toxin A #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Wolecule type: DNA
A;Residues: 1-2,'I',4-249,'R',251-254,'I',256-280 <SAK>
A;Cross-references: GB:M20371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 155.5; DB 1;
Pred. No. 0.00084;
5; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: staphylococcal serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 224-240 <BAI>
R; Sakurai, S.; Suzuki, H.; Kondo, I.
Cen. Microbiol. 134, 711-717, 1988
A; Title: DNA sequencing of the eta gene oc
A; Reference number: A46569; MUID:89036121
A; Accession: A46569
A;Reference number: A26680; MUID:87307959
A;Accession: A26680
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24.7%;
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Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : : | | : | |
62 NLPKELFSKVDEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 TAAFVEFINYAK 300
                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-280 <0T0>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                            A; Molecule type: DNA
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154
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                                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Staphylococcus aureus
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 18-Jun-1999
C; Accession: A26680; C26680; A26679; S11541; A46569
C; Accession: A26680; C26680; A26679; S11541; A46569
R;Lee, C.Y.; Schmidt, J.J.; Johnson-Winegar, A.D.; Spero, L.; Iandolo, J.J.
J. Bacteriol. 169, 3904-3909, 1987
A;Title: Sequence determination and comparison of the exfoliative toxin A and toxin B ge
                                                                                                                                                                                                                                                                                                                                                                    able serine proteinase VCA0803 [imported] - Vibrio cholerae (strain N16961 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                        Jecies: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                                                        RSI-ROVTNLTGTTIKISGYPGDKMRSTGKVSQ-WEMSGPVTREDTNLAYYTIDTFSGNS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 TNTRVAPYNSIA-----YITFGGSSCTGTLIAPNKILTNGHCVY-NTATRSYSAKGS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 ---FTGP-----QIGSTRNSTCSGDSGPVYWDSGSGYVQIGITSFGPSTC-GNPALPV 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYPGMND-STAVNGS---ANMTEFYVPSGYINTGASQY--DFAVIK--TDTNIGNTVG-- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YRSIRQ------VINLTGTTIKI-----SGYPGDKMRSTGKVS 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 NSSINNSYDENGTYKAIGHGYVNGNVAGGTRLLETTLTFVPFATCSAYYGANL-GPGHVC 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QWEMSGPVTREDTNLAYYTIDTFSGNSGSAML-DQNQQIVGVHNAGYSNGTINGGP--KA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
59
  KIDNTLQYPYSTSAMVLSKYYGVADGMNVEGRGSANFIKDNVLITAAHNYYR---HDYGK
                                          KGS---VYPGMNDSTAVNGSANMTEFYVPSGYINTG---ASQYDFAVIKTDTNIGNTVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 TNANVANYPSFASLAIYISPYQYSSGTYCGATVLNSRYILTAAHCIYGNSYTMLYTV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 156; DB 2; Length 330
28.0%; Pred. No. 0.00096;
ive 27; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epidermolytic toxin A precursor - Staphylococcus aureus
                                                                                                                                                                                                                  GSAMIDQNQQIVGVHNAGYSNGTINGGPKATAAFVEFI 296
                                                                                                                                                                                                                                               N; Alternate names: exfoliative toxin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.0
Best Local Similarity 28.0
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TSVFTEVSDY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TAAFVEFINY 298
                                            147
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Search completed: June 21, 2002, 18:42:41
Job time: 125 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLPFI 197
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                                                                  RESULT 13
889765
hypothetical protein 22592 [imported] - Escherichia coli (strain 0157:H7, substrain EDL9 C:Species: Escherichia coli (croate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C:Accession: E85765
R:Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew N:Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew N:Derna, A.; Grotheek, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, N:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-273 <STO>A; Residues: 1-273 <STO>A; Cross-references: GBARE005174; NID:912515576; PIDN:AAG56585.1; GSPDB:GN00145; UWGP:225 TPerimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C., ACCESSION: H64915
R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CG.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Title: The complete genome sequence of Escherichia coli K-12.
A,Reference number: A64720; MUID:97426617
A,Reference number: A64720; MUID:97426617
A,Residues: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-273 <BLAT>
A,Residues: 1-273 <BLAT>
A,Cross-references: GB.AE000255; GB.U00096; NID:91787875; PIDN:AAC74670.1; PID:91787882; C;Reywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ie: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 31-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 IAPNLALTAGHCLLTPPKGKADKAVALRFVSNKGLWRYDIHDIEGRVDPTLGKRLKADGD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYI-TFGGSSCTGTL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1APNKILTNGHCVYN-----TATRSYSAK------GSVYPGMNDSTAVNGS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 ANMTEFYVPSGYINTGASQYDFA-VIKTDTNIGNTV-----GYRSIRQVTNLFGTTIKI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 G----WIVP-----PAAAPWDFGLIVLRNPPSGITPLPLFEGDKAALTAALKAAGRKVTQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 SGYPÇDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAML---DQNQQIVGVH 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVAKSANDEVSTL-----FFGHDDRVPVNDTTQSPWDAVGQLETASGNLCTATL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.9%; Score 154; DB 2; Length 273; Best Local Similarity 23.6%; Pred. No. 0.001; Matches 57; Conservative 40; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cies: Escherichia coli
----VGIGNYVK 272
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265
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Gaps

43;

9.8%; Score 153.5; DB 2; Length 273; 24.6%; Pred. No. 0.0011; tive 37; Mismatches 89; Indels 43

Conservative

Best Local Similarity Matches 55; Conserva

Query Match

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Firettellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S. on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzanson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Mor A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumonia A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005672; PIDN:AAK74556.1; PID:g14971860; GSPDB:GN00164; TI
A;Experimental source: strain T1GR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        choline binding protein G [imported] - Streptococcus pneumoniae (strain TIGR4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: C95045
181
                                                                                                                                                                                                                                        182 QYDFA-VIKTDTNIGNTV-----GYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 TGTLIAPNKILTNGHCVYNTATRSYSAKGS---VYPGMNDSTAVNGSANMTEFYVPSGYI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 NTG---ASOYDFAVIKTDTNIGNTVGYRSI-RQVTNLTGTTIKISGYPGDKMRSTGKVSQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 -WEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SANFIKDNVLITAAHNYR----HDYGKEADDIYVLPAVSPSQEPFGKIKVKEVRYLKEFR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                           92 GKADKAVALRFVSNKGLWRYEIHDIEGRVDPTLGKRLKADGDG-----MIVP-----PAAA
                                                                                                                        -----TATRSYSAK------GSVYPGMNDSTAVNGSANMTEFYVPSGYINTGAS
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                                                                                                                                                                                                                                                                                                                                                           235 MSGPVTREDTNLAYYTIDTFSGNSGSAML----DQNQQIVGVHNA 275
                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 153.5; DB 2; 27.0%; Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94;
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 21, 2002, 18:42:21 ; Search time 13.5 Seconds (without alignments) 866.171 Million cell updates/sec US-09-652-743A-12 1559 1 MKKVKKLIPSLLVFGALSVP......NGGPKATAAFVEFINYAKAQ 302

Title: Perfect score: Sequence: ing table:

105224 seqs, 38719550 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P80057 bacillus li	P39790 bacillus su	PO4188 staphylococ			P09332 staphylococ				P24664 saccharopol			-				P36102 saccharomyc	Q03155 escherichia	P05805 bos taurus	P49863 homo sapien	P22698 dictyosteli		P14914 rickettsia		P42278 drosophila		P23605 lonomia ach	P00805 escherichia	P45508 escherichia		PO4949 escherichia		P15921 rickettsia
		 																1	-	-														
SUMMARIES	ID	GSEP_BACLI	MPR_BACSU	STSP_STAAU	ETA_STAAU	YDGD_ECOLI	ETB_STAAU	OMPB_RICJA	TRY3_AEDAE	YF48_MYCTU	TRYP_SACER	TRYP_FUSOX	SERI_BOMMO	TRY2_DROME	HYPA_HYPLI	YE59_MYCPN	TRYZ_DROER	PAN3_YEAST	AIDA_ECOLI	CAC3_BOVIN	GRAK_HUMAN	SPG7_DICDI	SLAP_ACEKI	120K_RICRI	OMPB_RICRI	TRYT_DROME	YK82_YEAST	ACH2_LONAC	ASG2_ECOLI	YFAL_ECOLI	YNR6_YEAST	FLIC_ECOLI	Y4FB_RHISN	OMPA_RICRI
	DB	-	7	-	-	Н	-		-	-	٦	7	٦	7	٦	7	7	-	-	-	7	7	_	٦	-	-	7	-	П	-	-	-	-	г
	Query Match Length	316	313	336	280	273	277	1656	254	678	227	248	389	280	256	269	281	619	1286	253	264	532	762	1300	1654	262	1169	214	348	1250	636	497	664	2249
æ	Query Match	27.0	18.0	12.2	10.0	9.8	8.5	7.9	7.7	7.6	7.6	7.6	7.5	7.4	7.3	7.2	7.2	7.2	7.1	7.1	7.0	7.0	7.0		7.0					6.9	•	•	6.8	6.8
	Score	420.5	280.5	189.5	155.5	153.5	133	123	120	119	118.5	118	116.5	116	113.5	113	112	112	111	110	109	109	109	108.5	108.5	108	108	107.5	107.5	107.5	107	106.5	106	106
	Result No.	C	) <sup>7</sup>	3	4	2	9	. ,	80	<b>о</b>	10	11	12	13	14	15	16	17	18	19	20	21	22	23	<b>54</b>	25	56	27	28	29	30	31	32	33

										P12021 sus scrofa	
DROME	ACHLY	CHLPN	MYCPN	HUMAN	YEAST	_TRIGA	SALTY	EURMA	_DROME	PIG	OMPB_RICCN
SER3	API_/	PM11	X321	MAS2	EGT2	VSP1_	BIGA	EUM3	SER1	APMU	OMPB
г	_	Н	7	7	7	Т	7	7	Н	Н	г
272	653	928	1005	989	1041	258	1953	261	265	1150	1655
6.7	6.7	6.7	6.7	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.4
105	105	105	105	103.5	103	102.5	101.5	101	101	101	100.5
			_	m	_	0	_	~	m		

## ALIGNMENTS

RESULT 1 GSEP_BACL1 ID GSEP_BACL1 STANDARD; PRT; 316 AA.	AC P8UUS/; D1-MAY-1992 (Rel. 22, Created) D7 01-MAY-1993 (Rel. 27, Last sequence update) D7 16-OCT-2001 (Rel. 40, Last annotation update) DE Glutamyl endopeptidase precursor (EC 3.4.21.19) (Glutamate specific CN B Endopeptidase) (GSE).			•	RL BUT. J BIOCHEM. 2041:163-171(1992).  CC -1-FUNCTION: SPECIFIC FOR HYPROLYSIS OF PEPTIDES BONDS ON THE CARBOXYL SIDE OF ACIDIC AMINO ACID RESIDUES, WITH A STRONG CC PREPERENCE FOR GLU.  C -1- CATALYTIC ACITIVITY: Preferential cleavage: Asp-1-xaa, Glu-1-xaa.  CC -1- SUBCELLULAR LOCATION: Secreted.  CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS THE	This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imposfied and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to licenseeisb-sib.ch).	EMBL; D10060; BAPIR; S23078; S23 PIR; A45134; A45 MEROPS; S01.271; InterPro; IPR001 InterPro; IPR001 Pfam; PF00089; t PRINTS; PR0089; SMART; SM00020;
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SEQUENCE
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                                                                                                                                                                                                                                                     SSIGSCTGWMIGPKTVATAGHCIYDTSSGSFAGTATVSPGRNGTSYPYGSVKSTRYFIPS 180
                                                                                                                                                                                                                                                                                                                      233 WEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQO-----IVGVHNAG-YSNGTIN 283
                                                                                                                                                                                                                                                                                                                                MEDLINE-90130256; PubMed-2105291;
Sloma A., Rudolph C.F., Rufo G.A. Jr., Sullivan B.J., Theriault K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haga K., Liu H., Yasumoto K., Takahashi H., Yoshikawa H.;
"Sequence analysis of the 70kb region between 17 and 23 degree of the
                                                                                                                                                                                                     ---PSSFDKVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYIT 113
                                                                                                                                                                                                                       GLYSKAFTGTGKVNET-KEKAEKKSPAKAPYSIKSVIGSDDRTRVTNTTAYPYRAIVHIS 120
                                                                                                                                              Gaps
                                                                                                                                                                                  61
                                                                                                                                                                5 KKLIPSLLVFGALSVPSFA---HAASDSVLTSDYDMVTSDG--KVISSADFHNDMKT---
                                                                                                                                                                            114 FGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPS
                                                                                                                                                                                                                                                                                           GYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT-NLTGTTIKISGYPGDKMRSTGKVSQ
                                                       SIMILARITY). SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ally D., Pero J.;
"Gene encoding a novel extracellular metalloprotease in Bacillus subtilis.";
                                                                                                                                             29;
                                                                                                                           DB 1; Length 316;
                                                                                                                          27.0%; Score 420.5; DB 1; Length 33.0%; Pred. No. 4.1e-23; ive 55; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular metalloprotease precursor (EC 3.4.21.-).
                                                                                             33611 MW; 96D7552CB7089B09 CRC64;
                                             GLUTAMYL ENDOPEPTIDASE.
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                    protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 172:1024-1029(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome.
V8_HIS; 1.
V8_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-68 FROM N.A.
                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                            30
94
316
141
261
142
279
                                                                                             316 AA;
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                                                                                                                                   al Similarity
101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus subtilis.
                    Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subtilis
                                                                                                                                                                                                                                                                                                                                                           284 GGPKAT 289
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RGTRIT 301
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01-FEB-1995
                   Hydrolase;
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                                                                                                                                                                                                                                                                                                                                                                                                                              MPR_BACSU
P39790;
                                             CHAIN
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus
                                                                                                                           Query Match
                                                                                    DISULFID
                                                                                              SEQUENCE
                                                                                                                                     Best Local
Matches 10
                             SIGNAL
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MPR_BACSU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith H., de Jong A., Bron S., Venema G.; regions selected from the characterization of signal-sequence-coding regions selected from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SIAY----ITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDST 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 AVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVTNLT--GTTIKI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSFDKVDDLSST---IGEKVKPL----TTYLKDFQT----KVVIGDDGRTKVTNTRVAPYN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 KLVPRFRKQWFAYLTVLCLALAAAVSFGVPAKAAENPQTSVSNTGK----EAD-----ATK 53
                                                                                                                                                                                                                                                                                                                                                      -:- SUBCELLULAR LOCATION: Secreted.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS THE
VB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CAUTION: CALLED "METALLOPROTEASE", BUT CLEARLY BELONGS TO THE FAMILY OF SERINE PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR METALLOPROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                         Saxild H.H., Jacobsen J.H., Nygaard P.; "Functional analysis of the Bacillus subtilis purT gene encoding formate-dependent glycinamide ribonucleotide transformylase."; Microbiology 141:2211-2218(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal; Zymogen; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.0%; Score 280.5; DB 1; Length 313; 29.4%; Pred. No. 3.6e-13; tive 50; Mismatches 129; Indels 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPYEG -> PLESTAQA (IN REF. D41788E8D652AE94 CRC64;
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                                                                                                                                                                                                           MEDLINE-96118702; PubMed-7496533;
MEDLINE-89108019; PubMed-3145906;
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                                                                            Bacillus subtilis chromosome.
Gene 70:351-361(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L10505; AAA22604.1; -.
EMBL; AB006424; BAA33121.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M22916; AAA22832.1; -. EMBL; Z99105; CAB12018.1; -.
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SWART; SMO0020; TYP_SPC; 1.
PROSITE; PSO0672; VB_HIS; 1.
PROSITE; PSO0673; VB_EBE; 1.
Hydrolase; Serine protease;
                                                                                                                                                          OF 1-10 FROM N.A.
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InterPro; IPR000126; Ser
Pfam; PF00089; trypsin;
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146
267
147
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MEROPS; S01.272; -.
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Best Local Simi
Matches 96;
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                                                                                                                                                                                                                                            20-MAR-1987 (Rel. 04, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Glutamyl endopeptidase precursor (EC 3.4.21.19) (Staphylococcal serine proteinase) (V8 proteinase) (Endoproteinase Glu-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rice K., Peralta R., Bast D., de Azavedo J., McGavin M.J.;
"Description of staphylococcus serine protease (ssp) operon in
Staphylococcus aureus and nonpolar inactivation of sspA-encoded serine
                                  230 TGFPCDKTFGT----MWSDTKPIRSAETYKLTYTTDTYGCQSGSPVYRNYSDTGQTAIAI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- CATALYTIC ACTIVITY: Preferential cleavage: Asp-|-Xaa, Glu-|-Xaa, -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS THE VB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The primary structure of staphylococcal protease.";
Can. J. Blochem. 56:534-544(1978)
-1- FUNCTION: PREFERENTALLY CLEAVES PEPTIDE BONDS ON THE CARBOXYL-
TERMINAL SIDE OF ASPARTATE AND GLUTAMATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carmona C., Gray G.L.; {\tt ^{N}UCleotide} sequence of the serine protease gene of Staphylococcus
SGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAML----DQNQQIVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WWW-"http://www.worthington-biochem.com/manual/P/STAP.html".
                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Firmicutes, Bacillus/Clostridium group, Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE: NAME-Worthington enzyme manual;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4ydrolase; Serine protease; Zymogen; Signal.
                                                                                                                                                                                                            336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 15:6757-6757(1987).
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InterPro; IPR001254; Trypsin.
                                                                          HNAGYSNGTINGGPKATAAFVEFINY 298
                                                                                                            HTNGGS -- SYNLGTRVTNDVFNNIQY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-20569178; PubMed-11119502;
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MEDLINE-87316953; PubMed-3306605;
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Drapeau G.R.;
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MEROPS; S01.269; -.
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PRINTS; PR00839; V8PROTEASE.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_SER; 1.
                                                                                                                                                                                                            STANDARD;
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P04188;
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STSP_STAAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| :: :||| | | | :: | :| | | | : | 104 ASGVVVGKDTLLTNKHVVDATHGDPHALK--AFPSAINQDNYPNGGFTAEQITKYSG--- 158
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J. Bacteriol. 169:3904-3909(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 VDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITF----GGSS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 CTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYP-GMNDSTAVNGSANMTEFYVPSGYIN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 ----MWESKGKITYLKGEAMQYDLSTTGGNSGSPVFNEKNEVIGIHWGGVPN-EFNG--- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KVSSLFVATLTTATLVSSPAANALS------SKAMDNHPQQTQSSKQQ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Exfoliative toxin A precursor (EC 3.4.21.-) (Epidermolytic toxin A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 TGASQYDFAVIKTDTNIGN-----TVGYRSIRQVTNLTGTTIKISGYPGDKMRST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | |::| | | : | | | | : | | | : | | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | | : | | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                    MISSING (IN REF. 3).
MISSING (IN REF. 3).
N -> D (IN REF. 3).
V -> T (IN REF. 3).
D -> N (IN REF. 3).
EFN -> QPD (IN REF. 3).
EFN -> QPD (IN REF. 3).
W; 8B138D0C7996AA3E CRC64;
                                                    SLUTAMYL ENDOPEPTIDASE
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                                                                          CHARGE RELAY SYSTEM.
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NCBI_TaxID=1280;
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  POTENTIAL.
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MEDLINE=87307960; PubMed-3040667;
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MEDLINE-87307959; PubMed-3040666;
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Best Local Similarity 24.2
Matches 74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ASQYDFAVI--KTDTN---IGNTVGYRSIRQVTNL-TGTTIKISGYPGDKMRSTGKVSQW 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GAGVDLALIRLKPDQNGVSLGDKISPAKIGTSNDLKDGDKLELIGYPFDH-----KVNQM 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 EMSG-PVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGYSN----GTINGGPKA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209 HRSEIELTTLSRGLRYKGF-TVPGNSGSGIFNSNGELVGIHSSKVSHLDREHQINYG--- 264
                                                                                                                                                                                                                                                                                                                                                                                              2 KKVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMV-TSDGKVISSADFHNDMKTPSSF 60
                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2B; ALSO KNOWN AS THE
V8 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-KIZ / MGIGS5;
MEDLINE-974266J7; Pubmed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Sho Y.;
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASE.
PROSITE; PS00672; V8_HIS; 1.
PROSITE; PS00673; V8_EBE; 1.
Hydrolase; Serine protease; Calcium; Toxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                          DB 1; Length 280;
                                                                                                                                                                                                                                           4FBAF750FFE43586 CRC64;
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                                                                                                                              EXFOLIATIVE TOXIN A. CHARGE RELAY SYSTEM. CHARGE RELAY SYSTEM. CHARGE RELAY SYSTEM.
                                                                                                                                                                                                                                                                                                        10.0%; Score 155.5; DB 1; 24.7%; Pred. No. 0.00025; ive 46; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative protease ydgD precursor (EC 3.4.21.-).
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                                                                                                                                                                                                                                           280 AA;
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 77; Conserv
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InterPro; IPR001254; Trypsin.
    Bacteriol. 169:3910-3915(1987)
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                                                                                          MEDLINE-89036121; PubMed-3183619;
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EMBL; M17347; AAA26625.1; -.
EMBL; L25372; AAA17490.1; -.
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1EXF; 25-FEB-98.
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PIR; S11541; S11541.
                                                 SEQUENCE FROM N.A.
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MEDLINE-90351379;
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MEDILINE-66277939; PubMed-3733674;
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Jackson M.P., Iandolo J.J.;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Exfoliative toxin B precursor (EC 3.4.21.-) (Epidermolytic toxin B).
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PUTATIVE PROTEASE YDGD.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CGRCD018A59DBC62 CRC64;
    and for
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                                                                            EMBL; AE000255; AAC74670.1; -.
MEROPS; S01.260; -.
BEGGENE; EG13925; ydgD.
InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR000124; Trypsin.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hypothetical protein; Hydrolase; Serine protease; Signal;
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    Usage
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223 CH
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CHARGE RELAY SYSTEM (BY SIMILARITY).
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                                               serine residue of epidermolytic toxin A.";
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(Rel. 40, Last annotation update)
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PIR; B26680; PRSAEB.
PIR; A26050, A26050.
HSSP: P09331; 1AGJ.
MEROPS; S01.270; -.
InterPro: IPR0001254; Trypsin.
Pfam: PF00089; trypsin. 1.
PRINTS; PR00873; V8PROTEASE.
PROSITE; PS00672; V8_HIS; I.
PROSITE; PS00673; V8_ERS; I.
Hydrolase; Serine protease; Toxin; S19
                                                                                                                                                MEDLINE-90346117; PubMed-2384148;
PubMed=2117445;
                                                                     Biochem. J. 269:535-537(1990).
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                        Bailey C.J., Smith T.P.; "The reactive serine res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NGFIQ--VSDKSFATVKA-INIGDGQFMFNTNATNANALNLQAGGTINFNGTDG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TGRLVLLSKNGAAT---DFNVT-----GSLGGNLKGIIELNTVAINGQLIA--NAGP 317
Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (Tompa) (Confedins: 120 kDa surface-exposed protein (Surface protein (romp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : :|: :| :: ||: ||: ||: |
PNAVITANANNGINLNTPAGSFNGLFLSNANNLAVTVSEDTTLGFINNAANNANRFNLTL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 VIGDDGRT-----KVTNTR-----VAPYN------SIAYITFGGSSCT- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---DAGKTLTITGQGITNVQSAATHNAQNIVAKFNGGAAIAMNDLSGLGTIDFGAAASTL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....-GTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 VFDLANPTTQKAPLILADNALIVNG----------ANGTLNVT- 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKMRSTGKVSQWEMSGPVTREDTNLAYYIDTFSGN-SGSAMLDQ----NQQIVGVHNAGY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 -KVISSADFHN--DMKTPS-SFD-----KVDDLSSTIGEK-----VKPLTTYLKDFQTKV 88
                                                                                                                                                                                                                                                                                    FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVTNLT-----GTTIKISGYPG
                                                                                                                                                                      Uchlyama T.; *Sequencing of the gene encoding the protein rOmp B of Rickettsia ^{\ast}
                                                                                                                                                                                                                                                                                                          SUBCELLUIAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED LAYER WITH HEXAGONAL SYMMETRY.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140;
                                                                                                                                                                                                               Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROPEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 KDA SURFACE-EXPOSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 123; DB 1; Length 1656;
                                                                      Rickettsia japonica.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.3%; Pred, No. v.**; vative 52; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 533 POLY-GLY.
1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 VKKLIPSLLVFG--ALSVPSFAHAASDSVL----TSDYDMVTSDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SN---GTINGGPKATAAFVEFINYAKA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR003858; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall.
CHAIN 1338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB003681; BAA20138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 23.3
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1656
                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1339
                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
ACTIVATION PEPTIDE.
TRYPSIN 3AI.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
REQUIRED FOR SPECIFICITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                      "Isolation, sequencing and characterization of two cDNA clones coding for trypsin-like enzymes from the midgut of Aedes aegypti."; Insect Mol. Biol. 2:71-79(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANM-TEFYVPS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Xaa, Lys-1-Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Extracellular.
-i- TISSUE SPECIFICITY: MIDGUT.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                    MEDLINE-97242546; PubMed-9087545;
Kalhok S., Tabak L.M., Prosser D.E., Brook W., Downer A.E.R.,
                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%; Score 120; DB 1; Length 254; 25.5%; Pred. No. 0.073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Zymogen; Digestion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43AAF13B8DE7D485 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 0.073;
                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00020; Tryp_SPC; 1.
PROSITE: PS50240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
PROSITE: PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Signal; Zymog
                                                                                                                     Trypsin 3Al precursor (EC 3.4.21.4).
Aedes aegypti (Yellowfever mosquito)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
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2009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene family
SIGNAL
                                                                                                                                                                                                                                            NCBI_TaxID=7159;
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28
68
1113
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                                                                                                                                                                                                                                                                                                                                                                    White B.N.;
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TRY3_AEDAE
P29786;
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CONTRACTOR CONTRACTOR CONTRACTOR

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Hypothetical
TRANSMEM
                                                                                                                                                                                 Query Match
Best Local Simi
Matches 80;
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                                                                                CONFLICT
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                                                     TRANSMEM
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TRYP_SACER
                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98295987; PubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elgimeier K., Gas S., Bary C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oldrer S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                         174 GYINTGASQYDFAVIKTDTNIGNTVGYRSIRQV-----TNLTGTTIKISGYPGDK---
                                                                                                                                                                                 -----MRSTG--KVSQWEMSG------PVTREDINLAYYI--IDIFSGNSGSAMLDQNQQ
                                                                                                                                                                                                                                  160 EMNTLLRAVNVPSYNQAECAAALVNVVPVTEQMICAGYAAGGKDSCQGDSGGPLV-SGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculist; Rv1548c; -
InterPro; IPR002989; Mycobact_pentapep.
InterPro; IPR000030; PPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE007026; AAK45866.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01469; Pentapeptide_2; 13. Pfam; PF00823; PPE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
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STRAIN-CDC 1551 / Oshkosh;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                        219 LVGVVSWG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YF48_MYCTU
                                                                                                                                                                                 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 FGALSVPS----FAHAASDSV--LTSDYDMV----TSDGKVISSADFHNDMKTPSSFDKV 63
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-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Xaa, Lys-1-Xaa.
-!- MISCELLANEOUS: HARDLY AUTOLYZES ITSELF AT ALL AT ITS ACTIVE PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTK-----VTNTRVAPYNSIAYITFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 439 GELSTGIGNSGQLSTGWFNSATTSTGWFNSGTTNTGWFNSGTTNTGIG--NS-----GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 NLVTGSM----GLFNSGH----TNTGSFNA-GSM-----NTGDFNSGNVNTGYFNSGNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 NTGASQYDFAVIKTDTNIG--NTVGYRSIRQVTNLTG---TTIKISGYPGDKMRSTGKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 536 NTGF-----FINSGDLNTGLFNSVNQPVQNSGWLHTGTNNSGYANAGTFNSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 QWEMSGPVTREDTNLAYYTIDTFSGNSGSAML-DQNQQI--VGVHNAGYSNG--TINGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92176171; PubMed-1794983; "Amaner T., Kobuke M., Tsutsui H., Toida T., Sakiyama T., Sakiyama Y., Sakiyama F., Saki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miyamoto K., Matsuo H., Narita K.;
(In) Dai 30 kai tanpakushitsu kouzou touronkai kouen youshishuu,
pp.77-80 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nagamine Y., Norioka S., Sakiyamam F.;
Unpublished results, cited by:
Yamane T., Robuke M., Tsutsui H., Toida T., Suzuki A., Ashida
Kawata Y., Sakiyama F.;
Biochem. 110:945-950(1991).
                                                                                                                                                                                                                                                                                                                                                                                            7.6%; Score 119; DB 1; Length 678; 25.7%; Pred. No. 0.29; tive 41; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAV-1995 (Rel. 32, Last senotation update)
01-MOV-1995 (Rel. 32, Last annotation update)
Trypsin (EC 3.4.21.4) (SET).
Saccharopolyspora erythraea (Streptomyces erythraeus).
Batteria; Firmicutes; Actinobacteridae;
Actinomycetales; Pseudonocardineee; Pseudonocardiaceee;
Transmembrane; Complete proteome.
                                                                                                                                                                D -> G (IN REF. 2).
209F1593D52533A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 AA.
                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
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                                                     34 PO
200 PO
258 D
66736 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            630 -- TANISGEVN 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 KATAAFVEFIN 297
                                                                                               180
258
678 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharopolyspora.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                resolution.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 YINTGASQYDFAVIKTDTNI--GNTVGYRSIRQVTN--LTGTTIKISGYPG-DKMRSTGK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 VSQWEMSGPVTREDTNLAYYTI-------DTFSGNSGSAMLDQNQQIVGV 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 Y---SGNNNDLAILKLSTSIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGGSSTP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSANMTEFYVPSG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.6%; Score 118; DB 1; Length 248; 21.7%; Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 REQUIRED FOR SPECIFICITY. 24576 MW; 1A0EBA88C3E70294 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-CGT-2001 (Rel. 40, Last annotation update)
18-cirin precursor (Silk gum protein).
Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 HNAGYSNG----TINGGPKATAAFVEFIN-YA 299
                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYPSIN.
                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001314; Chymotrypsin.
Interpro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Middle silk gland;
MEDLINE=83082839; PubMed=6294094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                         EMBL; S63827; AAB27568.1; -. PDB; 1TRY; 01-JAN-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
108
204
66
189
          TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 MEROPS; S01.103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
26
65
108
204
50
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ACT_SITE
ACT_SITE
ACT_SITE
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SERI_BOMMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REQUIRED FOR SPECIFICITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 VVIGDDGRTKVTNTRVAPYNSIAYITFGGSS-CTGTLIAPNKILINGHCVYNTATRSYSA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 KGSVYPGMN-DSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNI-----GN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDT-NLAY--YT--- 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 DAGYAPDTAATILGWGNTSEGGQQADHLQ-----KATVPVNSDDTCKQAYGEYTPNA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of inhibited trypsin from Fusarium oxysporum at 1.55 A.";
Acta Crystallogr. D 51:73-84(1995).
-!- CATALITY Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
HSSP; P20231; JAAO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY [1.8 ANGSTROMS). MEDLINE-93324511; PubMed-8332590; Rypniewski W.R., Hastrup S., Betzel C., Dauter M., Dauter Z., Papendorf G., Branner S., Wilson K.S.; The sequence and X-ray structure of the trypsin from Fusarium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
NCBI_TaxID=5507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.6%; Score 118.5; DB 1; Leuye...
of 0%; Pred. No. 0.082;
......hes 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rypniewski W.R., Dambmann C., von der Osten C., Dauter M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D5AC5E47B227B418 CRC64;
                                                                                                                                                                                                                                                                                                                                           SYSTEM.
SYSTEM.
SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 -----IDTFSGNSGSAMLDQNQQIVGVHNAG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 MVCAGVPEGGVDTCQGDSGGPMV-VNNKLIGVTSWG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-EDC-1998 (Rel. 37, Last annotation update)
Trypsin precursor (EC 3.4.21.4).
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                                                                                                                                                                                                                                                                                                                                           CHARGE R
CHARGE R
CHARGE R
                                                                                                       InterPro; 1PR001314; Chymotrypsin. InterPro; 1PR001254; Trypsin. Pfan, PR00089; trypsin, 1. PRINTS; PR00722; CHYMOTRYPSIN. SWART; SM00020; Tryp_SPC; 1. PROSITE; PS50240; TRYPSIN_DOM; 1. PROSITE; PS00135; TRYPSIN_HIS; 1. PROSITE; PS00135; TRYPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23308 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusarium oxysporum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AA;
                                                                                    MEROPS; S01.102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson K.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRYP_FUSOX
P35049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxysporum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
    01-NOV-1995 (Rel. 32, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update)
                                Trypsin zeta precursor (EC 3.4.21.4).
                                                            Drosophila melanogaster (Fruit fly).
                                                                                                                NCBI_TaxID=7227;
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                                             TRY-ZETA.
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                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.ch.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMN----DSTAVNGS 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SASYSSSSSSTEESSSSSRAASSTDASSNTDSNSNSAGSSTSGGRRTYGYSSNSRDGS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 VSTTGSSSNTDSNSVGSRRSGGSSSHEDSSKS--RDENVSTTGSSSNTDSNSVGSS 281
                                                                                                                             gland of Bombyx mori.";
Blochimie 68:1165-1173(1986).
-1- FUNCTION: PROVIDES THE SILK FIBROIN THREAD WITH A STICKY COATING.
-1- FUNCTION: PROVIDES THE SILK FIBROIN THREADS TOGETHER.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: PRODUCED EXCLUSIVELY IN THE MIDDLE (MSG)
SECTION OF SILK GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
Okamoto H., Ishikawa E., Suzuki Y.; Structural analysis of serior genes. Homologies with fibroin gene for the 5' flanking nucleotide sequences."; Biol. Chem. 257:15192-15199(1982).
                                                                                  MEDLINE-87076763; PubMed-3024742;
Michaille J.J., Couble P., Prudhomme J.-C., Garel A.;
"A single gene produces multiple sericin messenger RNAs in the silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVFGALSVPSFAHAASD----SVLTSDYDMVTSDGKVIS-----SADFHNDMKTPSSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LIALALSVKAFGHHPGNRDTVEVKNRKYNAASSESSYLNKDNDSISAGAHRAKSVEQSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 ANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN------TVGYRSIRQVTNLTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 IKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 VS-----STGSSS----NTDSNSSNAGSSTSGGSSTYGYSS----NSRDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 389;
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: BA605BC0305EAF19 CRC64;
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                                                                                                                                                                                                                                                                                                                                                      EMBL, J01029; -; NOT_ANNOTATED_CDS.
EMBL, J01031; -; NOT_ANNOTATED_CDS.
EMBL, J01031; -; NOT_ANNOTATED_CDS.
EMBL, J01032; -; NOT_ANNOTATED_CDS.
EMBL, J01033; -; NOT_ANNOTATED_CDS.
EMBL, J01034; -; NOT_ANNOTATED_CDS.
EMBL, M26101; AAA27843.1; -.
EMBL, M26102; AAA27844.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 NA-----GYSNGTINGGPKATAA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38820 MW;
                                                                        SEQUENCE OF 317-354 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 20.7%;
watches 67; Conservative
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389
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P42280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 LKDFQTKVVIGDDGRT---KVTNTRVAPYN-SIAY--ITFGGS----SCTGTLIAPNKIL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 TNGHCVYNTATRSYSAKGSVYPGMNDSTAVNG-SANMTEFYVPSGYINTGASQYDFAVIK 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 VDPPLALNNFTIRGIKLASEQPIEGTVSKVSGWGTTSPG-----GYSSNQLLAVDVPIV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                 Wang S., Magoulas C., Hickey D.A.;
Submitted (JAN-1994) to the EMBL/Genenkal databases.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Xaa, Lys-1-Xaa.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 TDTNIG-NTVGYRSIRQVTN--LTGTTIKISGY----PGDKMRSTGKVSQWEMSGPVTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Zymogen; Signal; Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 DINLAYYIIDTFSGNS---GSAMLDQNQQIVGVHNAGYSNGTINGGPKA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 SNELCDQDYEDFGDETYRITSAMLCAGKP--GVGGADACQGD-SGGPLA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REQUIRED FOR SPECIFICITY 6255F1CCEAE823CB CRC64;
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CHARGE RELAY SYSTEM
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TRYPSIN ZETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIYBSSS: FBGT0011556; Try-zeta.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
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Best Local Similarity 27.5
Matches 63; Conservative
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87
134
234
88
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                                                                                                                                                                             TRYPSIN FAMILY.
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SEQUENCE FROM N.A.
                                 STRAIN-OREGON-R;
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39
87
134
234
72
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72
230
238
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D -> P (IN REF. 3).
L -> W (IN REF. 2).
63D12D337F66AA61 CRC64;
                                                      7.3%; Score 113.5; DB 1; 22.7%; Pred. No. 0.21; tive 42; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                        569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000036; AAB96030.1; ALT_INIT.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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569 H
25 N
63118 MW;
                        27907 MW;
                                                                               Conservative
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51
248
51
248
256 AA;
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                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
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P75324;
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SEQUENCE
CONFLICT
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SEQUENCE
                                                        Query Match
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                                                                     Local
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CHARGE DEPORT SPECIFICITY (BY SIMILARITY).
S -> M (IN REF. 3).
Q -> E (IN REF. 3).
                                                                                                                          Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Oestridae; Hypoderma.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 31-51.
MEDLINE-8123292; PubMed-7018579;
Tong N.T., Imhoff J.M., Lecroisey A., Keil B.;
"Hypodermin A, a trypsin-like neutral proteinase from the insect Hypoderma lineatum.";
                                                                                                                                                                                                            B, C in larval
                                           193587; 025080; 01-30. Created)
01-JUN-1994 (Rel. 29, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-HWY-2000 (Rel. 36, Last annotation update)
Hypodermin A precursor (EC 3.4.21.) (HA).
Hypoderma lineatum (Barly cattle grub) (Common cattle grub).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                        SEQUENCE OF 3-256 FROM N.A.
Kuhn I., Files J.G., Pruett J.H., Temeyer K.B.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIVATION PEPTIDE.
                                                                                                                                                                                                Moire N., Bigot Y., Periquet G., Boulard C.; "Sequencing and gene expression of hypodermins stages of Hypoderma linearium"; MOI. Biochem. Parasitol. 66:233-240(1994).
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                                    256 AA
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PRINTS; PR00722; trypsin; I.
PROSTE; SM0020; Tryp_SPC; I.
PROSITE; PS50240; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_RIS; I.
Hydrolase; Serine protease; Zymogen
                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-95107346; PubMed-7808473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001314; Chymotrypsin
Interpro; IPR001254; Trypsin.
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                                    STANDARD;
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72
230
204
37
45
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MEROPS; S01.111; -.
                                                                                                                                                   NCBI_TaxID=7389
                                    HYPA_HYPLI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                          14;
                                                                                                                                                          66 LSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIA 125
                                                                                                                                                                                                                                                                                                                                                                      63 KNVIITAAHCLRNVVAEELRVRVGSSYWEHGGSL----RNISKFQIHESYVEP-TKEYD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVIKTDINIGNIVGYRSIRQVIN-----LIG---TIIKISGYPGDKMRSIG-KV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 VALLKLDSDLSFNSTIKAI-ELTNEIPPEYADAIVSGWGETLVPPPGIP-DQLRSVDVKI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 SQWEMSGPVTRE---DINLAY-----YTI--DIFSGNSGSAMLDQNQQIVGVHN 274
                                                                                                                                                                                                                                                                                                                        126 PNKILTNGHCVYNTATRSYSAK-GSVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYD 184
                                                                                                                                                                                                                24 LSQSDGRIVGGVESKIEDFPWQISLQRDGR-----------HYCGGSIXS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
-!- SIMILARITY: STRONG, TO THE N-TERMINAL SECTION OF M.PNEUMONIAE MPN456 AND M.GENITALIUM MG321.
                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
Length 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL LIPOPROTEIN MPN459.
N-ACYL DIGLYCERIDE (POTENTIAL).
ICE6F077E15B13F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MPN459 precursor (H08_orf591).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Lipoprotein; Membrane; Signal;
Complete proteome.
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                                                                                                                                                                                                        122 TLIAPNKILTNGHCVYNTATRSYSAKGSVYPCHNDSTAVNGSANMTEFVVPSGYINTGAS 181
                                                                                                                                                                                                                           98 ------TSVKGYKKKTSTASNMK-TASVSSSSSTG------NNGST 131
                                                                                                                                      62 KVDDLSSTIGEKVKPLTTYLKDFQTKVVIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTG 121
                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 113; DB 1; Length 569;
Best Local Similarity 21.2%; Pred. No. 0.62;
Matches 60; Conservative 43; Mismatches 96; Indels 84; Gaps
                                                                                         2 KKVKKLIPSLLVFGALSVPSFAHAASDSVLTSDYDMVTSDGKVISSADFHNDMKTPSSFD 61
                                                                                                                                                                                                                                                                                                                                              241 REDTNLAYYIDT --- FSGNSGSAMLDQNQQIVGVHNAGYSNG 280
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Search completed: June 21, 2002, 18:46:01 Job time: 220 sec

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Sequence 2, App Sequence 4, App Sequence 4, App Sequence 121, App Sequence 121, A Sequence 121, A

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Sequence Sequence Sequence Sequence

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Sequence 27, Appl Patent No. 5248599

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Title: Perfect score:

Sequence:

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Run on:

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Minimum DB Maximum DB

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ADDRESSEE: No. 55232370 No. 5523237disk of No. 5523237th America, Inc. STREET: 405 Lexington Avenue, 62nd Floor
CITY: New York
STATE: New York
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COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/090,048
FILING DATE: 16-JUL-1993
CLASSIFICATION A435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 199/91
FILING DATE: 06-FEB-1991
PRIOR APPLICATION NUMBER: PCT/DK92/00036
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: A9715, Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3396.214-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 405.5; DB 1;
Pred. No. 3e-29;
               US-08-553-516-2

US-08-238-130-2

US-08-238-130-2

US-08-816-915-4

US-08-906-769-121

US-08-906-769-121

US-08-906-616-121

US-09-012-692-121

US-09-012-692-121

US-09-012-692-121

US-08-906-613-121

US-08-906-129-5

US-08-908-682-128-5

US-08-908-682-128-5

US-08-908-682-128-5

US-08-908-682-128-5

US-08-908-682-128-5
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APPLICANT: Nielsen, Per M.
TITLE OF INVENTION: PROTEIN PREPARATIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States of America
ZIP: 10174-6201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08090048; Patent No. 5523237; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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39.3%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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(without alignments)
568.738 Million cell updates/sec
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                                                                                                                                                                                                                                                                           ......NGGPKATAAFVEFINYAKAQ 302
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                                                                                                                                               June 21, 2002, 18:38:51; Search time 12.97 Seconds
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Compugen Ltd.
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US-09-012-431-83
US-09-012-692-83
US-08-906-613-83
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US-08-657-192-3

US-08-657-192-9

US-08-657-192-9

US-08-657-192-9

US-08-657-192-15

US-08-657-192-15

US-08-523-373-23

US-08-914-235-32

US-09-314-235-33

US-09-314-235-33

US-09-314-235-33

US-09-072-384-18

US-09-072-384-15

US-09-072-384-15

US-09-072-384-15

US-09-072-384-15

US-09-072-384-15

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US-09-072-384-15
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-08-817-795-83
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                                                                                                                                                                                                                                                                                                                                                                                      231628 seqs, 24425594 residues
                    GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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1559
1 MKKVKKLIPSLLVFGALSVP.
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seq length: 2000000000
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Match Length
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405.5

Score 405.5

Result

129.5 129.5 121.5 121.5 120

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89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKG 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDONQ 267
                                     149 SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT- 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: No. 58663570 No. 5866357disk of No. 5866357th America 405 Lexington Avenue
                                                                                                               208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 405.5; DE Pred. No. 3e-29;
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                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lumer...
APPLICANT: Mortensen, Steen
APPLICANT: Budtz, Peter
APPLICANT: Eriksen, Svend
APPLICANT: Friksen, Svend
TWENTION: Protein Hydrolysates
                                                                                                                                                                                       268 Q----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                            3396.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/927,661A
FILING DATE: 31-AUG-1992
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07927661A Patent No. 5866357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Sco:
39.3%; Pre-
tive 36;
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TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Agris, Cheryl H
REGISTRATION NUMBER: 34,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 222 amino acids TYPE: amino acid
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Best Local Similarity 39.3%
Matches 83; Conservative
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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US-07-927-661A-1
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                                                                                                                                                                                                                                                                                                    US-07-927-661A-1
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                                                                                                                                      208 NLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYTIDTFSGNSGSAMLDQNQ 267
                                                                                                                                                                                                                89 VIGDDGRTKVTNTRVAPYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKG 148
                                                                                                               149 SVYPGMNDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTNIGNTVGYRSIRQVT- 207
                                                            Length 222;
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   77; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Danbmann, Claus
APPLICANT: Budtz, Peter
APPLICANT: Mortensen, Steen B.
TITLE OF INVENTION: A PROCESS FOR PRODUCING CHEESE
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.0%; Score 405.5; DB 2; 39.3%; Pred. No. 3e-29; ive 36; Mismatches 77;
     36; Mismatches
                                                                                                                                                                                                                                                                   268 Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/927,624
FILING DATE: 31 AUG 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DK91/0068
FILING DATE: 8 MAR 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/292,550
FILING DATE: 18 AUG 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                               uence 1, Application US/08292550 cent No. 5863573
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0298
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 39.3%
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Gregg, Valeta A. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
     83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-292-550-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
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       Matches
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PROCESS FOR PRODUCTION OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       3: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
                                                                     Sequence 5, Application US/08523373 Patent No. 6037145
                                                                                                     GENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
ITILE OF INVENTION: PROCESS FI
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
                                                                                                                                                                                                                                                                                                             ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 25.3%
Matches 57; Conservative
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                                                                                                                                                                                                                                                      CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                  USA
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US-08-523-373-6
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121 SLVGTTVTISGYPGDKTAGT----QWQHSGPIAISETYKLQYAMDTYGGQSGSPVFEQSS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 KVVIGDDGRTKVTNTRVAPYNSIAYITF----GGSSCTGTUIAPNKILTNGHCVYNTATR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SYSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN-- 196
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MUTANT STAPHYLOCOCCUS AUREUS V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.8%; Score 184; DB 1; 25.3%; Pred. No. 6.5e-09;
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches
                                                                            268 Q-----IVGVHNAG-YSNGTINGGPKAT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
TELECOMUNICATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                Sequence 3, Application US/08657192
Patent No. 5747321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                PROTEASES
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.8%
Best Local Similarity 25.3%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Virginia
COUNTRY: United States
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                                                                                                                                                                                                                                        APPLICANT: YABUTA, MAS
APPLICANT: OHSUYE, KAZ
TITLE OF INVENTION: MU
TITLE OF INVENTION: PH
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 IGEVVKPATMSNNAETQVNQ----NITVTGYPGDKPVAT----MWESKGKITYLKGEAMQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 KVVIGDDGRTKVTNTRVAPYNSIAYITF ---- GGSSCTGTLIAPNKILTNGHCVYNTATR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 EVILPNNDRHQITDTINGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLINKHVVDATHGD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 SYSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN-- 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Score 184; DB 3;
5; Pred. No. 6.5e-09;
41; Mismatches 83
                                                                                                                                                                                                                                  001560-251
                                                FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
                                                                                                                                                                        NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET UNBER: 001
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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25.3%;
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87 KVVIGDDGRTKVTNTRVAPYNSIAYITF----GGSSCTGTLIAPNKILTNGHCVYNTATR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 SYSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN-- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAY 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 184; DB 1; Length 532; 25.3%; Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Patent No. 6037145
GENERAL INFORMATION:
APPLICANT: Vabuta, Masayuki
APPLICANT: Ohsuye, Razuhiro
ITILE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 YTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
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MUTANT STAPHYLOCOCCUS AUREUS V8
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLING DATE: 03-JUN-1996
                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 001560-264 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                               PROTEASES
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            532 amino acids
                                                                                                                                                                        STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meuth, Donna M. REGISTRATION NUMBER:
APPLICANT: OHSUYE, KAZU
TITLE OF INVENTION: MUT.
TITLE OF INVENTION: PRO
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                      CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 SYSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN-- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAY 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.8%; Score 184; DB 3; Length 392; 25.3%; Pred. No. 7.7e-09; tive 41; Mismatches 83; Indels
                                                                 APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazubiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 YTIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIF: 22314-3187

ZIF: 22314-3187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT AFPLICATION NUMBER: US/08/523,373
PELING DATE: 05-SEP-1995
CLASSIFRCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 36,607
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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Patent No. 5747321
  Sequence 6, Application US/08523373 Patent No. 6037145
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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APPLICANT: YABUTA, Masayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 amino acids
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Best Local Similarity 25.3%
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide US-08-523-373-6
                                                                                                                                                                                                              Alexandria
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                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                       STATE: VA
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87 KVVIGDDGRTKVTNTRVAPYNSIAYITF----GGSSCTGTLIAPNKILTNGHCVYNTATR 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yabuta, Masayuki
APPLICANT: Ohsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCE: 24
CORRESPONDEMES ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 YIIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,192
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-170086
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 184; DB 1;
Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 11.8%; Score 184;
Best Local Similarity 25.3%; Pred. No. 1
Matches 57; Conservative 41; Mismatch
                                                                                                                                                                                                                                                                                 NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001560-264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/08523373 Patent No. 6037145 GENERAL INFORMATION:
                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 537 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-657-192-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
ZIP: 22313-1404
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 EVILPNNDRHOITDTTNGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLTNKHVVDATHGD 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SYSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN-- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAY 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 YIIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kazuhiro
MUTANT STAPHYLOCOCCUS AUREUS V8
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 184; DB 3;
Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: P.O. BOX 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    001560-251
                                                                                                                                                                                      FILING DATE: 05-SEP-1995
CLASSIFICATION: 435
TOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/08657192; Patent No. 5747321; GENERAL INFORMATION: APPLICANT: YABUTA, Masayuki; APPLICANT: OHSUTE, ARAUHITO TITLE OF INVENTION: PROTEASES; TITLE OF INVENTION: PROTEASES
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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25.3%;
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             532 amino acids
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Best Local Similarity 25.3%
Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703-836-2021
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: peptide US-08-523-373-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
COUNTRY: United S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
  Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                           22314-3187
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                                        USA
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88 VVIGDDGRTKVTNTRVAPYNSIAYITF----GGSSCTGTLIAPNKILTNGHCVYNTATRS 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSOWEMSGPVTREDTNLAYY 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 TIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 183; DB 3;
Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION C
WHUBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches
                                                           APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
    JP 6-238595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 24, Application US/08523373
; Patent No. 6037145
; GENERAL INFORMATION:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                               not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.7%;
Best Local Similarity 25.4%;
Matches 57; Conservative 40
                       07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-1995
                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                         214 amino acids
                                                                                                                                                                                          TELEPHONE: 703-000
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: peptide US-08-523-373-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-SEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                    linear
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ZIP: 22314-3187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-523-373-24
                                                                                                                                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 YSAKGSVYP-GMNDSTAVNG---SANWTEFYVPSGYINTGASQYDFAVIKTDTNIGN--- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.7%; Score 183; DB 3; Length 213; 25.4%; Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
APPLICANT: Yabuta, Masayuki
APPLICANT: Yabuta, Masayuki
APPLICANT: Obsuye, Kazuhiro
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 TIDTESGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 DLSTTGGNSGSPVFNEKNEVIGIHWGGVPN-EFNG----AVFI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Mismatches
                                                                                                                                                                                                                                               001560-251
                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-238595
FILING DATE: 07-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-296028
FILING DATE: 07-NOV-1994
ATORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/COCKET NUMBER: 001560-25
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
    APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/523,373
FILING DATE: 05-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23, Application US/08523373 —Patent No. 6037145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZUP: 22314-3187

ZIP: 22314-3187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBB PC compatible

COMPUTER: IBB PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                             not relevant
                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.48;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Conservative
                                                                                                                                                                                                                                                                                                          703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
Us-08-523-373-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 57; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05
CLASSIFICATION:
                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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219 YPGDKMRSTGKVSQWEMSG-PVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGY 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 YPGDKMRSTGKVSQWEMSG-PVTREDTNLAYYTIDTFSGNSGSAMLDQNQQIVGVHNAGY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 PYNSIAYITFGGSSCTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGMNDSTAVNGSA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 PYNTIGNVFVKGTSATGVLIGKNTVLTNRHIA--KFANGDPSKVSFRPSINTDDNGNTET 99
                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/09314235
Fatent No. 6338845
GENERAL INFORMATION:
TOTALE INFORMATION:
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1997-07-18
EARLIER FILING DATE: 1997-06-01
EARLIER FILING DATE: 1991-01-17
EARLIER PELLING DATE: 1991-01-17
EARLIER PELLING DATE: 1991-01-17
EARLIER FILING DATE: 1999-01-17
EARLIER FILING DATE: 1999-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 162; DB 4; Length 241; 30.0%; Pred. No. 3.9e-07; ive 26; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: TERMAN, DAVID S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILLE REPERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 34 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                      214 SHLDREHQINYG-----VGIGNYVK 233
                                                                                                                SN----GTINGGPKATAAFVEFINYAK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 SHLDREHQINYG-----VGIGNYVK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 33, Application US/08896933 Patent No. 6221351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureas US-09-314-235-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Conservative
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                                                                                                                                                                                                                                                         RESULT 14
US-09-314-235-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-896-933-33
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LENGTH: 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 YSAKGSVYP-GMNDSTAVNG---SANMTEFYVPSGYINTGASQYDFAVIKTDTNIGN--- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 HALK--AFPSAINQDNYPNGGFTAENITKY-----SGEGDLAIVKFSPNEQNKHI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 -----TVGYRSIRQVTNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYY 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GEVVKPATMSNNAETQVNQ----NITVTGYPGDKPVAT----MWESKGKITYLKGEAMQY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 NMTEFYVPSGYINTGASQYDFAVI -- KTDTN -- - IGNTVGYRSIRQVTNL -TGTTIKISG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 PYGEYEVKEILQEPFGAGVDLALIRLKPDQNGVSLGDKISPAKIGTSNDLKDGDKLELIG 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VILPNNDRHQITDTTNGHYAPVTYIQVEAPTGTFIASGVVVGKDTLLTNKHVVDATHGDP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 PYNTIGNVFVKGTSATGVLIGKNTVLTNRHIA--KFANGDPSKVSFRPSINTDDNGNTET 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 32, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
ILE REFERENCE: 09629/005002
URRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 162; DB 4; Length 241; 30.0%; Pred. No. 3.9e-07; ive 26; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 TIDTFSGNSGSAMLDQNQQIVGVHNAGYSNGTINGGPKATAAFV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 183; DB 3;
; Pred. No. 4.1e-09;
40; Mismatches 83
                                                  NAME: Meuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 001
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus aureas US-08-896-933-32
                                                                                                                                                                                                                                                                                 LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Juery Match
Best Local Similarity 25.4%;
Matches 57; Conservative 40
FILING DATE: 07-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 30.0%
Matches 62; Conservative
                                                                                                                                                 TELEPHONE: 703-650
TELPHONE: 703-650
TOTAL 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide > 18-523-373-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-896-933-32
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LENGTH: 241
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; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LEWGTH: 246
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
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	10;						
	Gaps	M 154	177	V 206	P 135	G 259	G 187
	36;	GSVYPG	2	YRSIRO	017G	TESGNS	TEVGNS
8.6%; Score 134; DB 4; Length 246;	best Local Similality 20.4%; Figu. NO. 0.00014; Matches 58; Conservative 27; Mismatches 83; Indels 36; Gaps	96 TKVTNTRVAPPNSIAYITFGGSS-CTGTLIAPNKILTNGHCVYNTATRSYSAKGSVYPGM 154	26 THITDNARSPYNSVGTVFVKGSTLATGVLIGKNTIVTNYH-VAREAAKNPSNI 77	155 NDSTAVNGSANMTEFYVPSGYINTGASQYDFAVIKTDTN-IGNTVGYRSIRQV 206	:	207 TNLTGTTIKISGYPGDKMRSTGKVSQWEMSGPVTREDTNLAYYIDTFSGNSG 259	136 ANIPOHIDIQKGDKYSLLGYPYNYSAYSLYQSQIEMFNDSQYFGYFEYGNSG 187
3 4; I	83;	NGHCVYN	NYH-VAF	FAVIKT	LAIIKL	SPVTREI	
134; DI	best Local Similarity 20.4%; Fred. No. 0.00014; Matches 58; Conservative 27; Mismatches 83	IAPNKILT	IGKNTIVT	IdDI	SPYGQGLDI	KVSQWEMS	YOSQIEM-
Score	27; Mis	S-CTGTL	TLATGVL	NTGAS	EAEEIKE	DKMRSTG	NYSAYSE
8.68;	20.4%; ative	AYITFGGS	GTVFVKGS	FYVPSGYI	i i i FPTPYGKF	IKISGYPG	YSLLGYPY
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Conserv	RVAPYNSI	ARSPYNSV	NGSANMTE	:	TGTT	IDIQKGDK
tch	58; 58;	TKVTNT	THITDN	NDSTAVI	: I IFTPAQI	TNL	ANIPDH
Query Match	tches	96	36	. 155	. 78	207	136
no or	Ma	0y	qq	Ļ.		οy	q

Search completed: June 21, 2002, 18:42:16 Job time: 205 sec

260 SAMLDQNQQIVGVHNAGYSNGTIN 283 | : ::|:|: | :| 188 SGIFNLKGELIGIHSG--KGGQMN 209

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